AR257466 LCU551424 PSVIC VFVIC LCU551425 AJ626897

891.2 750 468.6 465.8 461 455.4 AY500372 AJ626898

AR257466 Sequence
AJ551424 Lens culi
Y00722 Pisum sativ
Y00462 Vicia faba
AJ551425 Lens culi
AJ656897 Pisum sativ
AY60372 Lupinus a
AJ66898 Pisum sativ
AY80372 Lupinus a
AJ66898 Pisum sativ
AY808679 Clycine m
AR714521 Sequence
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AR714521 AB197786 AR714525 AR714526 AR714452 AR714451 BD175903

AR202568 AR486455 AR615272

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June 23, 2006, 09:32:31; Search time 11858.6 Seconds (without alignments) 10957.506 Million cell updates/sec
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Maximum Match 100%
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ALIGNMENTS

1 (bases 1 to 2032)

Burks, A.W. Jr., Stanley, J.S., Cockrell, G., King, N.E., Sampson, H.A., Helm, R.M. and Bannon, G.A.

Peanut allergens and methods
Patent: US 6486311-A 21 26-NOV-2002;

Putent: US 6486311-A 21 26-NOV-2002;

NY PAT 20-DEC-2002 ö 120 240 120 121 TGCCAAGTCATCACCTTACCAGAAGAAACAGAGAACCCCTGCGCCCCAGAGGTGCCTCCA 180 121 TGCCAAGTCATCATCACTTACCAGAAGAAAACAGAGAACCCCTGCGGCCCAGAGGTGCCTCCA 180 9 61 GGTTTCTCCACTGATGCTGTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA 61 GGTTTCTCCACTGATGCTGTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA GAGTTGTCAACAGGAACCGGATGACTTGAAGCAAAAGGCATGCGAGTCTCGCTGCACCAA AATAATCATATATTCATCATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGGAG .. 0 Length 2032; Indels linear DB 2; ö DNA Query Match
100.0%; Score 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches AR257469 Sequence 21 from patent US 64863111. AR257469 Location/Qualifiers
1. .2032
/organism="unknown"
/mol_type="genomic DNA" AR257469.1 GI:27307482 Unknown. Unclassified. . Unknown. 181 source DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS JOURNAL RESULT 1 AR257469 FEATURES TITLE ORIGIN LOCUS d 合 ò ò 8 ò

AR257469 Sequence
AR716329 Sequence
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SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. Unclassified. I (bases 1 to 2032) AUTHORS Dodo, H.W., Arntzen, C.J., Viquez, O.M. and Konan, K.N. TITLE Down-regulation and silencing of allergen genes in transgenic peanut seeds JOURNAL PATHORS DOS, 13-SEP-2005; PEATURES 1. 2032 //organism="unknown" ORIGIN	Duesty Match Bast Local Similarity 100.08; Pred. No. 0; No. 0; Indels 2013; Bast Local Similarity 100.08; Pred. No. 0; O. 1 Indels 2013; Bast Local Similarity 100.08; Pred. No. 0; O. 1 Indels 2013; Battches 2012; Conservative 0; Mismatches 0; Indels 0; Gaps 11 AATAITCATATATATATCATCAATCATCATTATAGAGAGAGAGAATCAGAGAGAG	TOTTCCCAAGCACGCTGATGCTGATACATCCTGTATCACGCACACCCACACACA

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1 (bases 1 to 2012)

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1 Usases 1 to 2012)

2 Cockrell, C. Stanley, J.S., Helm, R.M. and Bannon, G.A. Recombinant peanut allergen Ara h I expression and IgE binding in patients with peanut hypersensitivity
J. Clin. Invest. 96 (4), 1715-1721 (1995)
                                                                                                                               CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAAACAACCACAGAATCTTCCTTGC
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Original source text: Arachis hypogaea (strain Florunner)
Location/Qualifiers
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/strain="Florunner"
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Db	6 70 TION ION N DS	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 2041) AUTHORS Burks, A.W. Jr., Stanley, J.S., Cockrell, G., King, N.E., Sampson, H.A. Helm, R.M. and Bannon, G.A. TITLE Peanut allergens and methods JOURNAL Patent: US 6486311-A 23 26-NOV-2002,	Mt. Sinai School of Medicine and University of Arkansas; New York, FEATURES Location/Qualifiers source 12041 /organism="unknown" /mol_type="genomic DNA"	Query Match 100.0%; Score 2032; DB 2; Length 2041; Best Local Similarity 100.0%; Pred. No. 0; Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0	Qy 1 AATAATCATATATTCATCAATCATCTATAAAGTAGTAGGAGGAGGAGGGGGGGG	GGTTTCTCCACTGATGCTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA 	121 TGCCAATTCATCACCTTACCAGAAGAAAACAGAGAACCCTGCGCCCAGAGGTGCCTCCA 	GAGITGTCAACAGGAACGGATGACTTGAAGGCAAAGGCATGCGAGGTCTCGCTGCACCAA 	241 GCTCGACTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACACTGGCACCACCACCA [301 ACGTTCCCTCCAGGGAACGGAACGTGGCCGCCACCCGGAGACTACGATGACCG		Oy 421 AAGAGAAGACTGGAGACAACCAAGAAGATTGGAGGGACCAAGTCATCAGCAGCC 480	Qy 481 ACGGADATAAGCCCCGAAGGAAGAAGAACAACAAGAGTGGGGAACACCAGGTAGCCA 540
	961 GAGCAGCGGAGACCAATCATCTTGCAGGCTTCAGCAGGAATACGTTGGAGGCCGC 1020	1081 GCAAGAGGAGAGGGCGATGGAGTACTCGGAGTAGTGAGAACAATGAAGGAGT 1140	1201 AAAGAAAGGCTCCGAAGGAAGAAGGAAATATCACCAATCAAT	CCAGCTTCAGGACCTGGACCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTTGT	GCTCCCACACTTCAACTCAAGGCCATGGTTATCGTCGTCGTCACAAAGGAACTGGAAA 144	CCTTGAACTCGTGGCTGTAAGAAGAGCAACAACAGGGGGGGG	1501 GGACGAAGACGAAGAAGAGGAAGTAACAGAGAGGTGCGTAGGTACACACGAGGTT 1560 	1561 GAAGGAAGGCGATGTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAAGGCTTCCTC 1620 	CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAAACAACACAGGAATCTTCC 	1681 AGGTGATAAGGACAATGTGATAGACCAGATAGAGAAGCAAGGATTTAGCATTCCC 1740 	1741 TGGGTCGGGTGAACATGAGAAGCTCATCAAAAACCAGAAGGAATCTCACTTTGTGAG 1800 1741 TGGGTCGGTGAACAAGAGTTCAGAAACTCAAAAACCAAAAGGAATCTCACTTTGTGAG 1800	TGCTCGTCCTCAATCTCAATCTCCATCTCCGTCGTCTCCTGAGAAAGAGTCTCCTGAGAA 1	192

1261 GCCCGATCTTTTCTAACAACTTTGGGAGGTTATTTGAGGTGAAGCCAGAAGAAGGAGCTTTGAT 1390	RESULT 8 BD107898 LOCUS DEFINITION Methods and reagents for decreasing allergic reactions. ACCESSION BD107898.1 GI:23202716 VERSION BD107898.1 GI:23202716 VERSION BD107898.2 GI:23202716 VERSION BD107898.1 GI:23202716 VERSION BD107898.2 GI:23202716 VERSION BD107898.1 GI:23202716 VERSION BD107898.2 GI:23202716 VERSION COURCE Unidentified Unidentified Unidentified Unidentified Unidentified Unidentified Unidentified UNIVERSITY OF NEW YORK, HOWARD SOSIN COMMENT OS Arachis L. (Peanut) VINIVERSITY OF NEW YORK, HOWARD SOSIN COMMENT OS Arachis L. (Peanut) PR 22-JAN-2002 PF 29-JAN-1999 US 60/074624,13-FEB-1998 US 60/074633 PR
191 GAGTIGTCAACAGGAACCGGATGACTTGAACCAAAAGGCATGCGAGTCTCCCTCACCACCACACACA	961 GAGCAGCCGAGACCAATCATCCTACTTGCAGGGTTCAGCAGGAATACGTTGGAGGCCCC 1020 961 GAGCAGCCGAGACCAATCATCCTACTTGCAGGGATTCAGCAGGAATACGTTGGAGGCCGC 1020 961 GAGCAGCCGAGACCAATCCATCATCTTGCAGGGATTCAGCAGGAGTCGC 1020 1021 CTTCAATGCGGAATTCAATGAGATACGGAGGGTGTTGTTAGAAGAGAATGCAGGAGGTGA 1080 1021 CTTCAATGCGGAATTCAATGAGAGGGGTGGCGAGGAGGAGGAGGAGGAGGTG 1080 1021 CTTCAATGCGGAATTCAATGAGAGGGGTGGGTGATGAAGAGAATGAAGGAGGGGGG

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PT HAWADO SOSIN GARY A BANON, WESLEY A BIRX JR, HYU A SAMPTHON PC C12N15/09, A01H5/00, A01K67/027, A61K39/35, C07K14/435, PC C07K14/435, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/00, C12N15/00, C12N5/00, C12N15/00, C12N15/0
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PP 21-NOV-2001 JP 2001356754
PR 29-DEC-1995 US 60/009.455,04-MAR-1996 US 08/610.424 PI WESLEY A BURKS JR.RICKI M HELM,GAEL COCKRELL,STEVEN PI J STANLEY,GARY A BANNON
PC C12N15/09,A61X81/00,A61X81/00,A61X37/02
CC Strandedness: Double;
CC Topology: Linear;
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Bannon,G.A.
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                                                                            Gaps
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                                                   <u>DB</u>
                                                 88.8%; Score 1805.2;
95.2%; Pred. No. 0;
iive 0; Mismatches
DNA
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Best Local Similarity 95.2
Matches 1935, Conservative
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Arachis hypogaea
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae; Papilionoideae,
Aeschynomeneae, Arachis.
        GCTCCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCGTCACAAAAAGGAACTGGAAA
                                                                                                                                                                                                                                       GAAGGAAGCGATGTGTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCTC
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THE CITY UNIVERSITY OF NEW
                                                             CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGGATCAAAGAAGGAGCTTTGAT
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Patent: WO 0140264-A 5 07-JUN-2001;
Panacea Pharmaceuticals, LLC (US);
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Sequence 5 from Patent W00140264.
AX155332 GI:14536767
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TITLE
JOURNAL
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a & 6		AR257467 LOCUS DEFINITION Sequence 19 from patent US 6486311. ACCESSION AR257467 KERSION AR257467.1 GI:27307480	ear PAT 20-DEC-2002
2 & a	GCAAGAGGAGAGGCAAGGCGATGAGTACTCGGAGTAGTGAGAACAATGAAGGAGT 	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1949) AUTHORS Burks, A.W. Jr., Stanley, J.S., Cockrell, G., King.	J.N.E., Sampson, H.A.,
장 임 장	1141 GATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACGCTAAATCCGTCTC 1200 	Helm, R.M. and Bannon, G.A. TITLE Peanut allergens and methods JOURNAL Patent: US 648511-A 19 26-NOV-2002; Mt. Sinai School of Medicine and University of	Arkansas; New York,
상 원	1201 AAAGAAAGGCTCCGAAGAAGAGGGAGATATCACCAACCCAATCAACTTGAGAGAGA		
රු පු	1261 GCCCGATCTTTCTAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAGAACCC 1320 	genomic DNA"	Š
<u>ک</u> ج	1321 CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAGAAGCAGCTTTGAT 1380	Query Match Best Local Similarity 95.0%; Pred. No. 0; Matches 1894; Conservative 0; Mismatches 46; Indel	
िले	GCTCCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCGTCAACAAGGAACTGGAAA 14	Qy 48 CAATGAGAGGGAGTTTCTCCACTGATGCTTGCTAGGGATCCTTGTCCTGGCTTCAC 	CTTGTCCTGGCTTCAG 107
g & :	GCTCCCACACTICAACTCAAAGGCCAIGGICAICGICGICGICAACAAAGGAACAGAAAAAAAA	OY 108 TITCTGCAACGCATGCCAAGTCATCACCTTACCAGAAAACAGAACCCTGCGCCC	SAGAACCCTGCGCCC 167
g &	GCTTGAACTCCTAGCTGTAGCTGTAGCTGAACAACACACAC	Qy 168 AGAGGTGCCTCCAGAGTTGTCAACAGGAACGGATGACTTGAAGCAAAAGGCATGCGAGT	CAAAAGGCATGCGAGT 227
g &	S GGACGAAGACGAAGAAGAGGAAGGAAGTAACAGAGAGGTGCGTAGGTACACAGGGAGGTT 1 1 GAAGGAAGGCGATGTGTTCATCATGCAGCAGGTCATCAGTGAGCCATGAAGGCTTCCTC 1 1	Oy 228 CTCGCTGCACCAAGCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACTG	CCTCGAGGACACACTG 287 ACACTG 222
g &	GAAGGAAGGCGATGTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCTC CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAAACAACCACAGAATCTTCCTTGC	Qy 288 GCACCAACCAACCATCCCCTCCAGGGAGCGGACACGTGGCCGCCAACCCGGAGACT	CGCCAACCGGAGACT 347
g &	CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAACAACCACAGAATCTTCCTTGC AGGTGATAAGGACAATGTGATAGACCAGATAGAGAAGCAAGC	Qy 348 ACGATGATGACCGCGTCAACCCCGAAGAGGAAGGAGGCCGATGGGGACCAGCTGGAC C 283 ACGATGACGCCGTCAACCCCGAAGAGGAGGAAGGAGGCCGATGGGGACCAGCTGAAC	regegaccagcregac 407
a &	GGTGATAAGGACAATGTGATAGACCAGATAGAGAAGCAAGC	Qy 408 CGAGGGAGCGTGAAAGAGAAGAAGACTGGAGACAACCAAGAGAAGATTGGAGGCGACCAA	BATTGGAGGCGACCAA 467 BATTGGAGGCGACCAA 402
원 장	1715 TÖGTTCGGGTGAACATGAGAAGCTCATCAAAAACCACAAGAAGTCTCACTTTGTGAG 1774 1801 TGCTCGTCCTCAATCTCAATCTCCAATCTCCGTCGTCTCCTGAGAAAGAGTCTCCTGAGAA 1860	468	3AACAAGAGTGGGGAA 527
qa		DD 403 GICAICHACLAGCCACGAAAAAAAAAAAAAAAAAAAAAAAAAAAA	58
දු සු	1861 AGAGGATCAAGAGGAAGAAACCAAGGAGGGAAGGGTCCACTCCTTTCAATTTTGAAGGC 1920 	463	
ò	1921 TITTAACTGAGAATGGAGCAACTTGTTATGTATGGATAATAAGATCAGGCTTTTGTACT 1980	OY 588 GGCGGTTTAGCACCCGCTACGGGAACCGAAGCGTAGGGTCCTGCAGAGGTTTGCTGCAGGGTTTGCGGGAACCGGGAGGGTTGGGGGGGG	
8 &	98. TILIANCIGAGANIGGAGGANGTIGITATICATATATATATATATATATATATATATATATATAT	Qy 648 ACCAAAGGTCAAGGCAGTTTCAGAATCTCCAGAATCACCGTATTGTGCAGATCGAGGCCA	GTGCAGATCGAGGCCA 707
Db	1927 CTACTATCCAAAAACTTATCAATAAATAAAAGGTTTGTGCGTTGTTTCTCC 1978 12	Qy 708 AACCTAACACTCTTGTTCTTCCCAAGCACGCTGATGCTGATAACATCCTTGTTATCCAGC	ATCCTTGTTATCCAGC 767

, RESULT 12

Qy 1839 CTGAGAAAGAGTCTCCTGAGAAAGAGGATCAAGAGGAGAAACCAAGGAGGAGGGTC 1898 Db 1766 GTCTCCTGAAAAAGAGGATCAAGAGGAAACCAAGGAGGAGGTC 1815 Qy 1899 CACTCCTTTCAATTTTGAAGGCTTTTAACTGAGGATGGAGGAACTTGTTATGTATG	RESULT 13 AR629097 LOCUS DEFINITION Sequence 4 from patent US 6835824. ACCESSION VERSION AR629097.1 GI:59756571 VERYWORDS SOURCE Unknown. ORGANISM Unknown. TITLE Peanut allergens and methods JOURNAL TITLE Peanut allergens and methods JOURNAL TITLE Peanut allergens and methods University of Arkanass: Little Rock, AR	MK DB 2; Length 1949; 46; Indels 54; Gaps TRAGGGATCCTTGTCCTGGCTTCAG	1 CAATGAGGGAGGGTTTCTCCACTGATGCTTGGGATCCTTGTCCTGGCTTCAG 60 108 TTTCTGCAACGCATGCCAAGTCATCACCTAACCAGAAAACAGAGAACCCTGCGCCC 16	Db 175 CTCGCTGCACCAAGCTCGAGTATGATCCTCGTTGTGTCTATGACACTG 222 Qy 288 GCACCACCAACCAACGTTCCCCTCCAGGGAGCCGCCCCCCCC
Oy 768 PAGGGCAAGCCACGTGACCGTAGCAAATGGCAATAACAGAAAGAGCTTTAATCTTGACG 827 Db 703 AAGGACAAGCCACGTGACCAAATGGCAATAACAGAAAGAGCTTTAATCTTGACG 762 AB AAGGACAAGCCACGTGACCGTTCAATGCCAATAACAGCATTTAATCTTGAACTGCCATGACA 867 Qy 828 AGGGCCATGCACTCAGAATCCCATCCGGTTTCATTTCCTACATCTTGAATCGAATGACATGACA 822 Oy 888 ACCAGAAACTCCAAGATCACATCCATTCATTACAACACGCCAGTTTGAGG 947 Db 111111111111111111111111111111111111	Qy 1008 CGTTGGAGGCCGCTTCAATGCGGAATTCAATGGGATGCTGTTAGAAGAGA 1067 Db 943 CTTTGGAGGCCCTTCAATGCGGAATTCAATGAGATACGGAGGTGCTGTTAGAAGAGA 1002 Oy 1068 ATGCAGGAGGCCCTTCAATGCGGAATTCAATGAGATACTCGGAGTACTTGTAGA 1127 Db 1003 ATGCAGGAGGAGAGAGAGAGAGAGGAGAGGCGATACTCGGAGTACTCGGAGTAGTG 1059 Oy 1128 ACAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTACTCGGAGTACTCGGAGTAGTG 1059 Oy 1128 ACAATGAAGAGAGAATAGTCAAAGAGAGCAGAGAGAGTTACTAAGAACGTG 1187 Db 1060 ATAATGAAGAGATAAGTCAAAGAGACCAACGAGATATCACCAACCA	TGAGAGAAGGCGAGCCCGATCTTTCTAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAG 13 [1428 AAGGAACTGGAAACTTGAACTCGTGGCTGTAAGAAAAGAGACAACAGAGGGGACGGC 148 [1357 AAGGAACTGGAAACCTTGAACTGTAAGAAAGAGAGAGACAACAACAGAGGGGACGGC 148 1488 GGGAAGAAGAGGAGGACGAAGAAGAAGAGAGAGA	Oy 1599 CAGTAGCCATCACGCTTCCTCCCAACTCCATTGGCTTCGCTATCAACGCTCAAA 1658 Db 1537 CAGTAGCCATCCTCCCCAACTCCCATCTGGTTGGCTTCGCTTCGCTTCGCTTGAAA 1596 Oy 1659 ACAACCACAAATCTTCCTTCCCAACTCTGCTTGGTTAGACCCAGATAGAAAGCTTAA 1596 Oy 1719 ACAACCACAGAATCTTCCTTGCAGGTGATAAGACAATGTGATAGACCAGATAGAGAAGC 1718 Db 1597 ACAACCACAGAATCTTCCTTGCAGGTGATAGGACAATGTGATAGACCAGATAGAGAAGC 1656 Oy 1719 AAGCGAAGCATTTAGCATTCCCTGGGTGAACAAGTTCAGAAAACC 1778 Db 1657 AAGCGAAGGATTTAGCATTCCCTGGTTCGGGTGAACAAGTTCAAAAACC 1716 Oy 1779 AGCGAAGGAATTTAGCATTTGTGAGTGCTTCGGTCTCCAATCTCCAATCTCCAATCTCCGTCGTCTC 1838 Db 1777 AGAGGAATCTCACTTTGTGAGTGCTCGTCCTCAATCTCCAATCTCCATCTCCGTCCTC 1838 Db 1777 AGAGGAGTTCCACTTTGTGAGTGCTCGTCCTCCAATCTCCAATCTCCGTCCTC 1838 1717 AGAGGAGTTCCACTTTGTGAGTGCTCGTCCTCCAATCTCCAATCTCCGTCCTCTCTCT

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REEGGRWGPAEPREREREEDWRQPREDWRRPSHQQPRKIRPEGREGEQEWGTPGSSEVR
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Arachis hypogea (clone Pl7) Ara h I mRNA, complete cds.
L38853
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Arachis hypogaea (peanut)
Bukaryota, Mypogaea
Spermatophyta, Magnoliophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
Stosida, eurosida I, Fabales, Fabaceae, Papilionoideae,
Aeschynomeneae, Arachis.
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to mRNA.
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Burke, A.W., Cockrell, G., Stanley, J.S., Helm, R.M. and Bannon, G.A.
Recombinant peanut allergen Ara h I expression and IgE binding in patients with peanut hypersensitivity
Unpublished (1994)
           AAGCGAAGGATTTAGCATTCCCTGGTTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACC
                                                                                     ACAACCACAGAATCTTCCTTGCAGGTGATAAGGACAATGTGATAGACAGAGGAAGC
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Pred. No. 0;
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/gene="Ara h I"
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llarity 95.0%;
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                                                                                               GGTTTCTCCACTGATGCTGTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA
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PGSHVRLETSRNNPFYFPSRRFSTRYONGNGAIRVLORFDORSRQFORLONGNED
PGSHVTJULPRHADADNI LU YL QQQATVTVANGNNRKG FNLDBGHALAI PSGFISYI LIN
RHDNQNLRVAKI SMPVNT PGQFBDFFPASRDOSSYLQGFSRNTLEAAFNAEFNBIRR
VLLERNAGGEQEBEQQRRWSTRSSENNEGVI VKVSKCHVEBLTKHAKSVSKGSEBEG
DITNPINLRGGEDLSNNFGKL,FRYKDPKRNPQLQDLDMMLTCVEIREGALMLPHFNS
KAWYI VVVNKGTGNLELVARKEQQORGRREBEEBEDDEBEEGSNREVRRYTARLKGGD
VFINPAAHPVAINASSELLLGFGINAENNHI FLAGDKDNU I DQI BKQAKDLLFFGG
GEQVEKLI KNQKESHFVSARPQSQSQSPSSPBKESPBKEDQBEBNQGGKGPLLSILKA
                                                                                                                                                               Arachis hypogaea major allergen Arahl gene, complete cds.
AF432231
 2018
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SCQQEPDDLKQKACESRCTKLEYDPRCVYDPRGHTGTTNQRSPPGERTRGRQPGDYDD
DRRQPRREEGGRWGPAGPREREEEDWRQPREDWRRPSHQQPRKIRPEGREGEGEWGT
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                                                                                                                                                                                                                                                                                                                                                                                              major peanut
                  1. .2674
/organism="Arachis hypogaea"
/mol_type="genomic DNA"
/variety="F78-1339"
/db_xref="taxon:3818"
/db_xref="taxon:3818"
/piolu(<1. .911,883. .1058,1308. .1388,1463. .2674)
/product="major allergen Arahl"
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Direct Submission
Submitted (11-OCT-2001) Food and Animal Sciences, Alabama .
University, 4900 Meridian Street North, Normal, AL 35762,
Location/Qualifiers
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/codon_start=1</pre>
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Structure and organization of the genomic clone
allergen gene, Ara h 1
Mol. Immunol. 40 (9), 565-571 (2003)
14597159
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/protein_id="AAL27476.1"
/db_xref="G1:16612200"
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Pred. No. 0;
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Arachis hypogaea
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1182	TGTAAAATTTTATCTAATGGTTCATTTTTTTTTTTTGATACATGTTGGTCAGAATTTAAC 1241	
945	644	
1242	AAATTACTGGTCCTAGATTTTTCTTATATTCAATTCTCAATTATCATCTTACATGTTGCT 1301	
1302	AGGATTTCTTCCCGGCGAGCAGCCGAATCATCATCTACTTGCAGGCTTCAGC 1000	
1001	AGGAATACGTTGGAGGCCGCCTTCAAT1027 	
1028	GCGGAATTCAATGATAC 1046 	
1047 (GGAGGGTGCTGTTAGAAGAGAATGCAGGAGGTGAGCAGAGAGAG	
1107 0	GGAGTACTCGGAGTAGTGAGAACAATGAAGGGGGATAGTCAAAGTGTCAAAGGAGCACG 1166 	
1167	TTGAAGAACTTACTAAGGAGGGTAAATCGGTCTCAAAGAAAG	
1227 1	atatcaccaacccaatcaacttgagagaggggagcccgatctttctaacaactttggga 1286 	
1287	AGTTATTTGAGGTGAAGCCAGACAAGAAGAACCCCCAGCTTCAGGACCTGGACATGATGC 1346 	
1347 1	TCACCTGTGTAGAGATCAAAGAAGGAGCTTTGATGCTCCCACACTTCAACTCAAAGGCCA 1406	
1407 1	TGGTTATCGTCGTCACAACAAAGAACTGGAAACCTTGAACTGGGGGGGG	
1467 7	agcaacaacagagggacggcgggaagaagaggaggacgaagacgaagaggag	
1527 (GTAACAGAGAGGTGCGTAGGTACACCGAGGTTGAAGGAAG	
1587 (CAGCAGCTCATCCAGTAGCCATCAACGCTTCCTCCGAACTCCATCTGCTTGGCTTCGGTA 1646 	
1647 7	TCAACGCTGAAAACAACCAGGATCTTCCTTGCAGGTGATAAGGACAATGTGATAGACC 1706 	
1707 #	AGATAGAGAAGCAAGGATTTAGCATTCCTGGGTCGGGTGAACAAGTTGAGAAGC 1766 	

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	Description	Aaf90339 Peanut al	Abx70603 Peanut Ar	Adg27462 Peanut Ar	Adv97537 Peanut Ar	Adv97600 Peanut Ar	Aas08537 DNA encod	Aat76613 Peanut al	Aaz06382 Peanut al	Aat76612 Peanut al	Abx70604 Peanut Ar	Adv97536 Peanut Ar	Adg27463 Peanut Ar	Aas08539 Anaphylac	Adv97605 Peanut Ar	Abs55196 Glycine m	Acc49562 Mature be	Acc49561 FLAG-tagg	Aav17564 Coding se
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ACC49553	ABS55198	AAV17562	ADT17970	ABS55197	ADX14996	AAV17563	ADX13542	ADX13070	ADX31954	ADX13568	ADX32038	ADX31953	ADX13111	ADX13980	ADX14004	ADX13015	ADX13092	ADX12354	ADX32347	ADX13078	ADX13996	AAV42316	ADX13556	AAV42311	AAV42310	ADX13016
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20.0	19.9	19.9	19.9	19.8	19.2	16.0	14.4	13.8	13.7	13.7	13.1	13.0	12.8	12.2	11.5	10.6	10.6	10.6	9.6	9.5	8.2	7.9	7.8	7.7	7.5	7.0
406.8	404	404	404	402	390	324.2	293.4	279.8	279.4	279.2	267	263.8	260.4	247.8	233	214.8	214.8	214.8	199.6	186	167.2	160.2	158.2	157.4	152.6	141.8
19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Peanut; allergen; Ara hl P41B; transgenic plant; allergy; ss. Location/Qualifiers
676. 93
/*tag= a /note= "PCR amplified fragment" Peanut allergen Ara hl P41B cDNA. AAF90339 standard; cDNA; 2032 BP. (revised)
(first entry) Arachis hypogaea. Key misc_feature 11-SEP-2003 23-JUL-2001 AAF90339; RESULT 1 AAF90339

20-NOV-2000; 2000WO-US031657 99US-0167255P (UYAL-) UNIV ALABAMA A & M. WO200136621-A2 19-NOV-1999; 25-MAY-2001

Producing transgenic peanut plants that produce allergen-free seeds, useful in non-allergenic foods, by antisense or sense co-suppression of Viquez OM; Konan KN, allergen-encoding genes. Dodo HW, Arntzen CJ, WPI; 2001-355630/37.

Claim 20; Fig 5; 72pp; English.

The present sequence is that of peanut allergen Ara hl P41B cDNA. A

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portion of this gene is homologous to the corresponding region of the peanut allergen Ara hl P17 gene. This region has been PCR amplified, cloned in transformation vectors (pUC18 and pB14434) in sense and antisense orientations and used to down-regulate Ara hl P41B and Ara hl P17 allergens in peanut. This is an example of the method of the invention, which relates to the production of a peanut plant having reduced, or undetectable, allergenic protein (AP) content in its seed. A peanut plant cell is transformed with a DNA construct containing an antisense AP gene and/or sense AP gene, or their fragments, regenerated to plants, and fertile transgenic plants that produce seeds with reduced AP content are identified. The seeds are useful for preparation of allergen-free foods. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a modified anaphylactic food allergen has an amino acid sequence that is substantially identical to that of natural anaphylactic food allergen, except for a cysteine residue that has been modified so that it cannot participate in the disulphide bond. The modification may also comprise mutation of the IgE binding sites to reduce allergenicity. Also included are: (1) a method of making a modified anaphylactic food allergen; (2) a nucleotide molecule encoding or for causing a site specific mutation in the modified anaphylactic food allergen; (2) a transgenic plant or animal expressing the modified anaphylactic food allergen; (4) a method of treating an individual by reducing the clinical response to a natural anaphylactic food allergen is useful for preventing or treating allergen; anaphylactic food allergen is useful for preventing or treating allergic reactions associated with any natural allergen such as food, insect,
TTTTAACTGAGAATGGAGGAACTTGTTATGTATCGATAATAAGATCACGCTTTTGTACT 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caplan M, Sosin H, Sampson H, Bannon GA, Burks WA, Cockrell G;
Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;
Rabjohn PA, Shin DS, Stanley JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reactions associated with any natural allergen such as food, insect, rubber or preferably anaphylactic allergens. It is also useful for treating wounds in mammals such as bovine, canine, feline, caprine, ovine, porcine, murine or equine species. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified anaphylactic food allergen, useful for preventing or
treating allergic reactions associated with e.g. anaphylactic allergens.
                       Peanut, ss; allergy; Ara h1; Ara h2; Ara h3; gene; IgE binding site; anaphylactic food allergen; antiallergenic; vaccine; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2032 BP; 628 A; 473 C; 530 G; 401 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 10; 300pp; English.
                                                                                                                                                                                                                                           ВР
                                                                                                                                                                                                                                         ABX70603 standard; cDNA; 2032
                                                                                                                                                                                                                                                                                                                                                                          Peanut Ara h1 cDNA clone P41b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2001; 2001US-0276822P.
18-MAR-2002; 2002US-00276822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-2002; 2002WO-US009108
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Best Local Similarity 100.
Matches 2032; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypogaea.
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P-PSDB; ABU52412
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The invention relates to a modified anaphylactic food allergen whose amino acid sequence is substantially identical to that of a natural anaphylactic food allergen. The natural anaphylactic food allergen includes at least one cysteine residue that participates in a disulphide bond when the natural anaphylactic food allergen is in its native conformation, except that the cysteine residue has been modified so that it cannot participate in the disulphide bond. Also included are a method of making a modified anaphylactic food allergen, a nucleotide molecule encoding a modified anaphylactic food allergen, a nucleotide molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cockrell G;
RA, Maleki SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New modified anaphylactic food allergen comprising a cysteine residue which has been modified so that it cannot participate in the disulfide bond, useful for treating allergic reactions or wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RA,
          h3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burks AW,
i, Kopper
         Peanut; plant; ss; gene; allergen; Ara hl; Ara h2; Ara glycinin A2Bla; Jug n1; antiallergic; vulnerary; anaphylactic food allergen; IgE; allergy; wound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bannon GA, Bu:
RM, King NE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO 5; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sampson H, Eton C, Helm F
Stanley JS;
                                                                                                                                                        95US-0009455P.
96US-00717933.
96US-00717283P.
98US-0074624P.
98US-0074633P.
98US-00141220.
98US-00141220.
98US-00191593.
99US-00248673.
99US-00248673.
99US-0122452P.
99US-0122452P.
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99US-0122566P.
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Shin DS, Sta
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COCKRELL G.
COMPADRE C M.
CONNAUGHTON C.
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KING N E.
KOPPER R A.
MALEKI S J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sosin HB
                                                                                                                                                                                                                                                                                                                                                                                                                                         CAPLAN M J.
SOSIN H B.
SAMPSON H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-875632/81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHIN D S.
STANLEY J S.
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                                                            Arachis hypogaea
                                                                                     US2003202980-A1
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16-MAR-2001;
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23-SEP-1996;
31-JAN-1998;
13-FEB-1998;
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27-AUG-1998;
13-NOV-1998;
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Rabjohn PA,
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29-JAN-1
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(CONN/)
(HELM/)
(KING/)
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(COCK/)
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                                                  GATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACGCTAAATCCGTCTC
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                                                                                                    GCCCGATCTTTCTAACAACTTTGGGAAGTTATTTGAGGTGAAGGCCAGACAAGAAGAACCC
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             GCAAGAGAGAGGGCAGAGGCGATGGAGTACTCGGAGTAGTGAGAACAATGAAGGAGT
                                    GATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACGCTAAATCCGTCTC
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CTACTATCCAAAAACTTATCAATAAAATAAAAACGTTTGTGCGTTGTTTCTCC
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cuccleotide molecule for causing a site specific mutation in a gene encoding a natural anaphylactic food allergen, a transgenic plant or animal expressing a modified anaphylactic food allergen defined above, a method of treating an individual by reducing the clinical response to a natural anaphylactic food allergen and an isolated fragment of peanut allergen and an isolated fragment of peanut allergen and an isolated fragment of peanut allergen and Ara h 1, comprising at least 10 consecutive amino acids of ADG27464 or ADG27465. About 10-17% of the amino acids have been modified in at least one IGE epitope or all the IGE epitopes recognised when the natural anaphylactic food allergen is contacted with serum 19E from individual (s) allergic to the natural anaphylactic food allergen. The invention discloses Peanut allergens Ara h1, Ara h2, Ara h3 (and their encoding cDNAs), Soybean Glycinin A2B1a and IGE-binding epitopes of the English cannut allergen Jug n1. The modified anaphylactic food allergen can be used for treating allergic reactions or wounds. The present sequence encodes a Peanut allergen of the invention. 120 180 TGCCAAGTCATCACCTTACCAGAAGAAAACAGAGAACCCCTGCGCCCCAGAGGTGCCTCCA 180 240 240 360 420 480 480 540 540 900 99 780 420 600 9 AATAATCATATATATTCATCAATCATCAATAAGTAGTAGCAGGAGCAATGAGGAGGAGGAG TGCCAAGTCATCACCTTACCAGAAGAAAACAGAGAACCCCTGCGCCCCAGAGGTGCCTCCA GAGTIGICAACAGGAACCGGAIGACTIGAAGCAAAAGGCAIGCGAGTCCGCIGCACCAA GCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACACTGGCACCACCACCACCA ACGTTCCCCTCCAGGGGAGCGGACACGTGGCCGCAACCCGGAGACTACGATGATGACCG ACGTTCCCCTCCAGGGGGAGCGGACACGTGGCCCCCAACCCGGAGACTACGATGATGACCG ACGGAAAATAAGGCCCCGAAGGAAGAGAAGGAGAACAAGAGTGGGGAACACCCAGGTAGCCA CCGCTACGGGAACCAAAACGGTAGGATCCGGGTCCTGCAGAGGTTTGACCAAAGGTCAAG GCAGTTTCAGAATCTCCAGAATCACCGTATTGTGCAGATCGAGGCCAAACCTAACACTT AATAATCATATATATTCATCATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGGAG GGTTTCTCCACTGATGCTGTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA GAGTTGTCAACAGGAACCGGATGACTTGAAGCAAAAGGCATGCGAGTCTCGCTGCACCAA CCGTCAACCCCGAAGAGGAGGCCCGATGGGGACCAGCTGGACCGAGGGAGCGTGA CCGCTACGGGAACCAAAACGGTAGGATCCGGGTCCTGCAGAGGTTTGACCAAAGGTCAAG TGTTCTTCCCAAGCACGCTGATGCTGATAACATCCTTGTTATCCAGCAAGGCAAGCCAC AAGAGAAGAAGACTGGAGACAACCAAGAGAATTGGAGGCGACCAAGTCATCAGCAGCC **ACGGAAAATAAGGCCCGAAGGAAGAGAAGGAGAGACAAGAGTGGGGAACACCAGGTAGCCA** TGTGAGGGAAGAACATCTCGGAACAACCTTTCTACTTCCCGTCAAGGCGGTTTAGCAC GCAGTITCAGAATCTCCAGAATCACCGTATTGTGCAGATCGAGGCCAAACCTAACACTCT Gaps Length 2032; ö Sequence 2032 BP; 628 A; 473 C; 530 G; 401 T; 0 U; 0 Other; 0; Indels DB 10; 100.0%; Score 2032; 100.0%; Pred. No. 0; ive 0; Mismatches Query Match
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Matches 2032; Conservative 121 61 61 121 181 181 241 241 301 301 361 361 421 421 181 481 541 541 601 601 661 661 721 88888888888888888888888888 8 8 8 ò 셤 ઠે ద 6 B 6 පු 셤 8 6 8 6 6 6 g ò g Ś ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding peanut allergen Ara h 1, useful for obtaining diagnostics with optimal concentrations of each allergen, for developing panels of mixtures of recombinant allergens, and in immunotherapy.
                                                                                                                                                                                                                                                                                                                                  allergen; atopic dermatitis; diagnostic; immunotherapy; immediate type hypersensitivity; Ara h I; dermatological; antiallergic; immunosuppressive; antibody engineering; ss.
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This invention relates to a novel isolated nucleic acid molecule encoding the peanut allergen Ara h I that has been identified in patients with a tropic dermatitis. Specifically, it refers to a monoclonal antibody carpy enzyme-linked immunosorbant assay (ELISA) used to detect and quantify the peanut allergens, where the monoclonal antibodies have specificity for a selected peanut allergen antigen. The present invention also describes to hybridomas that produce two-site monoclonal antibodies specific for a peanut allergen that can be used in an ELISA to detect and determine the concentration of a specific peanut allergen in a food product or in food processing. Furthermore, it provides an expression vector and the isolated nucleic acid or its fraction can include a diagnostic label. Accordingly, these nucleic acids are useful for obtaining diagnostics with optimal concentrations of each allergen or for developing panels of mixtures of large numbers of recombinant allergens such that it can be used in immunotherapy for the treatment of food hypersensitivity candid survention.

Chord (PI) clone) of the invention.
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                                                                                                                                                    antiallergic;
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Best Local Similarity 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the coding sequence of anaphylactic antigen Ara h 1 is an anaphylactic antigen (A), which was used to design antigenic peptides having a reduced ability to bind immunoglobulin E (195) as compared with the intact (A), or having a sequence substantially identical to a portion of sequence of an antigen that includes at least one IgE binding site of the peptide is altered. The antigenic peptides are used in a composition which is useful for reducing risk or severity of allergic reaction to an antigen. This is done by identifying an individual at risk of allergic reaction to an antigen. Or an antigen, or a familial relationship with an individual who exposed to the antigen. Pervioually displayed allergic symptoms when exposed to the antigen. Collowing this an antigen-specific IgE present on one or more mast cells or basophils in the individual's serum is identified. The individual is which is selected with a peptide corresponding to a portion of the antigen, which is selected, formulated, and delivered so that binding of the peptide to antigen. Pervious is also useful for treating and manapose the converse of interact antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic fragments useful for reducing anaphylactic risk and reducing the severity and/or number of allergic symptoms in individuals sensitive to antigens, have reduced ability to bind Immunoglobulin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTTTCTCCACTGATGCTGTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA 120
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/transl_except= (pos:902. .904, aa:P
/product= "Peptide antigen Ara h 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caplan MJ, Sampson H,
                                                                                                                                                                                                                                                                                                                                                            (PANA-) PANACEA PHARM LLC.
(UYAR-) UNIV ARKANSAS.
(MOUN ) MOUNT SINAI SCHOOL MEDICINE NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2041 BP; 637 A; 473 C; 530 G; 401
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100.0%; Pred. No. 0;
iive 0; Mismatches
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing allergic reactions
                                                                                                                                                                                                                                                                                       2000US-0213765P.
2000US-0235797P.
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Matches 2032; Conservative (
                                                                                                                                                                                                                          06-DEC-2000; 2000WO-US033124
                                                                                                                                                                                                                                                                     99US-00455294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-381378/40.
P-PSDB; AAU04706.
                                                                                                                                 WO200140264-A2
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27-SEP-2000;
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This cDNA clone, designated P41b, codes for the major peanut allergen Ara hI (AAW22150), which has multiple IgE binding epitopes (see AAW24165-87). It was amplified from peanut seed cDNA using a primer (see AAT6616) based on an isolated Ara hI peptide (see AAW24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The gene is capable of producing a protein product in prokaryotic cells that is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hI and Ara hII (see AAW24164) can be used to raise monoclonal antibodies which are used in a specific two-site MAD ELISA for the detection of Ara hI or Ara hII (Claimed). IgE-binding Ara antigen epitopes may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock. (Updated on 17-OCT-2003 to standardise OS field)
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site monoclonal antibody based ELISA.
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Pred. No. 0;
0; Mismatches 4; :
                                                                                                                                                                                                                                                                                                  Stanley JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 31; Page 186-188; 354pp; English
                                                                                                                                                                                                                                                                                                  Cockrell G,
                                                                                                                                                                                95US-0009455P.
96US-00610424.
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Best Local Similarity 99.8%;
Matches 2028; Conservative
                                                                                                                                    96WO-US015222
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                                                                                                                                                                                                                                                      (UYAR-) UNIV ARKANSAS
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                                                                                                                                                                                                                                                                                                    Helm RM,
                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW22150
                                                                                                                                                                                29-DEC-1995;
04-MAR-1996;
                                           WO9724139-A1
                                                                                       10-JUL-1997
                                                                                                                                                                                                                                                                                                    Burks AW,
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                                                                                              TGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAGAAGGAATCTCACTTTGTGAG
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2005. .2010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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29-DEC-1997
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AGAGGATCAAGAGGAGAAAACCAAGGAGGAAGGGTCCACTCCTTTCAATTTTGAAGGC 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA clone, designated p17, codes for the major peanut allergen Ara hI (AAW22149), which has multiple IgE binding epitopes (see AAW24165-87). It was amplified from peanut seed cDNA using a primer (see AAT76616) based on an isolated Ara hI peptide (see AAW24206). The sequence shows significant homology with the vicilin family of seed storage proteins of other legumes. The gene is capable of producing a protein product in prokaryotic cells that is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hI and Ara hII (see AAW24164) can be used to raise monoclonal antibodies which are used in a specific two-site MAD BLISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara antigen epitopes may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                   Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody;
           AGAGGATCAAGAGGAGGAAAACCAAGGAGGAAGGCTCCATTCAATTTTGAAGGC
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                                                                                                           AAT76612 standard; cDNA to mRNA; 1949 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 31; Page 183-185; 354pp; English
                                                                                                                                                                                Peanut allergen Ara hI cDNA clone P17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           site monoclonal antibody based ELISA
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ELISA; analysis; Ara hI; ds.
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                                                 (UYAR-) UNIV ARKANSAS
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29-DEC-1997
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                                           54;
                                                                                      CAATGAGAGGGATTTCTCCACTGATGCTGTTGCTAGGGATCCTTGT
                                           Indels
                                             46;
Score 1752.4;
Pred. No. 0;
0; Mismatches
86.2%;
95.0%;
                                             Conservative
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(first entry)

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Peanut; ss; allergy; Ara h1; Ara h2; Ara h3; gene; IgE binding site; anaphylactic food allergen; antiallergenic; vaccine; wound healing.
                                                                                                                                                                                                                              Caplan M, Sosin H, Sampson H, Bannon
Compadre CM, Connaughton C, Helm RM,
Rabjohn PA, Shin DS, Stanley JS;
                                       Peanut Ara h1 cDNA clone P17.
                                                                                                                                                                           16-MAR-2001; 2001US-0276822P.
18-MAR-2002; 2002US-00276822.
                                                                                                                                                        18-MAR-2002; 2002WO-US009108
                                                                                                                                                                                                          (PANA-) PANACEA PHARM.
                                                                                         Arachis hypogaea
                                                                                                               WO200274250-A2.
                    26-MAR-2003
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ABX70604;
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ATGCAGGAGGTGAGCAAGAGGAGAGAGGGCAGAGGCGATGGAGTACTCGGAGTAGTGAGA 1127
         1060 ATAATGAAGGAGTGATAGTCAAAGTGTCAAAGGAGCACGTTCAAGAACTTACTAAGCACG
                                                                                             1128 ACAATGAAGGAGTGATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACG
                                                                                                                          TGAGAGGAGGCGCATCTTTCTAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAG
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                                                                                CTAAATCCGTCTCAAAGAAAGGCTCCGAAGAAGAGGGAGATATCACCAACCCAATCAACT
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GA, Burks WA, Cockrell G; King NE, Kopper RA, Maleki SJ;

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The invention relates to a modified anaphylactic food allergen has an amino acid sequence that is substantially identical to that of natural canaphylactic food allergen, except for a cysteine residue that has been modified so that it cannot participate in the disulphide bond. The modification may also comprise mutation of the IgE binding sites to comprise mutation of the IgE binding sites to complicate allergenicity. Also included are: (1) a method of making a complyactic food allergen; (2) a nucleotide molecule encoding or for causing a site specific mutation in the modified anaphylactic food allergen; (4) a method of treating an individual by reducing the clinical response to a natural anaphylactic food allergen; (4) a method of treating an individual by reducing the clinical response to a natural anaphylactic food allergen; (5) and an isolated fragment of peanut allergen such as 1 from allergen; con an anaphylactic food allergen is useful for preventing or treating allergic reactions associated with any natural allergens uch as food, insect, cubber or preferably anaphylactic allergens. It is also useful for treating wounds in mammals such as bovine, canine, feline, captine, covine, mutine or equine species. The present sequence is a cDNA concluding a peanut allergen (e.g. Ara hl, h2 or h3)
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                                                                                                         New modified anaphylactic food allergen, useful for preventing or
treating allergic reactions associated with e.g. anaphylactic allergens.
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Best Local Similarity 95.0%; Pred. No. 0;
Matches 1894; Conservative 0; Mismatches 46; Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1949 BP; 599 A; 455 C; 517 G; 378 T; 0 U; 0 Other;
                                                                                                                                                                                                                                        Example 3; Fig 11; 300pp; English.
WPI; 2003-018765/01.
                                      P-PSDB; ABU52413.
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ABX70604 standard; cDNA; 1949 BP

RESULT 10 ABX70604 ID ABX7 XX

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                                                                                                                                                                                                                                                                                                                                                             allergen; atopic dermatitis; diagnostic; immunotherapy; immediate type hypersensitivity; Ara h I; dermatological; antiallergic; immunosuppressive; antibody engineering; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peanut Ara h I allergen alpha P17 cDNA encoding a seed storage protein.
                                                                                                               AAGGAGCTTTGATGCTCCCCACACTTCAACTCAAAGGCCATGGTCATCGTCGTCGTCGAACA
                                                      AAGGAACTGGAAACCTTGAACTCGTAGCTGTAAGAAAAGAGCAACAACAACAGGGGGACGGC
                                                                            ------GTCTCCTGAAAAAGAGGATCAAGAGGAGGAAAACCAAGGAGGGAAGGGTC
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                                            AAGGAACTGGAAACCTTGAACTCGTGGCTGTAAGAAAAGAGCAACAACAGAGGGGACGGC
                                                                                              GGGAACAAGAGGAAGAAGAGGAAGATGAAGAGAGGAGGGAAGTAACAGAGAGG
                                                                                                                                                                                             AAGCGAAGGATTTAGCATTCCCTGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACC
                                                                                                                                                                                    ACAACCACAGAATCTTCCTTGCAGGTGATAAGGACAATGTGATAGACCAGATAGAGAAGC
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/transl_except= (pos: 1335. 1337; aa: Asn)
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                        ACGATGATGACCGCCGTCAACCCCGAAGAGGAGGAGGCCGATGGGGACCAGCTGGAC
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                                                                                                                      GTCATCAGCAGCCACGGAAAATAAGGCCCCGAAGGAAGAAGGAGGAGAACAAGAGTGGGGAA
                                                                                                                                CACCAGGTAGCCATGTGAGGGAAGAAACATCTCGGAACAACCCTTTCTACTTCCCGTCAA
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CTCGCTGCACCAAGCTCGAGTATGATCCTCGTTGTGTCTATG-
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New isolated nucleic acid encoding peanut allergen Ara h 1, useful for obtaining diagnostics with optimal concentrations of each allergen, for developing panels of mixtures of recombinant allergens, and in immunotherapy.
                                                                       Cockrell G,
                                                                                                                                               2; SEQ ID NO 4; 141pp; English
                                                                       Bannon GA,
                     98US-00191593
                                   95US-0009455P
96US-00717933
                                                                       Stanley JS,
                                                        (UYAR-) UNIV ARKANSAS
                                                                                     WPI; 2005-045982/05
P-PSDB; ADV97606.
                     13-NOV-1998;
                                   29-DEC-1995;
23-SEP-1996;
                                                                       Burks AW,
                                                                                                                                                Claim
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This invention relates to a novel isolated nucleic acid molecule encoding the peanut allergen Ara h I that has been identified in patients with a topic dermatitis. Specifically, it refers to a monoclonal antibody enzyme-linked immunosorbant assay (ELISA) used to detect and quantify the nary manual allergens, where the monoclonal antibodies have specificity for a selected peanut allergen antigen. The present invention also describes hybridomas that produce two-site monoclonal antibodies specific for a peanut allergen that can be used in an ELISA to detect and determine the concentration of a specific peanut allergen in a food product or in food processing. Furthermore, it provides an expression vector and the secondary processing. Furthermore, its fraction can include a diagnostic label. Accordingly, these nucleic acids are useful for obtaining diagnostics with optimal concentrations of each allergen or for developing panels of mixtures of large numbers of recombinant allergens such that it can be used in immunocherapy for the treatment of food hypersensitivity reactions. This polynuclecide sequence is the peanut Ara h I allergen con the invention.

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Gaps DB 14; Length 1949; 54; U; 0 Other; 46; Indels T, 0 Score 1752.4; Pred. No. 0; 0; Mismatches G; 378 Seguence 1949 BP; 599 A; 455 C; 517 Query Match 86.2%; Best Local Similarity 95.0%; Matches 1894; Conservative

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                                                                                                                                                          ACGATGATGACCGCCGTCAACCCCGAAGAGAGGAAGGAGGCCGATGGGGACCACCAGCTGAAC
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CAATGAGAGGAGGGTTTCTCCACTGATGCTGTTGCTAGGGATCCTTGTCCTGGCTTCAG
                                                                    TTTCTGCAACGCATGCCAAGTCATCACCTTACCAGAAGAAAACAGAGAACCCCTGCGCCC
                                                                                                                                      AGAGGTGCCTCCAGAGTTGTCAACAGGAACCGGATGACTTGAAGCCAAAAGGCATGCGAGT
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1487 1247 1307 1356 1007 1067 1002 1127 1059 1187 1236 1427 882 942 462 587 522 647 582 707 642 167 702 827 762 887 822 947 527 ACAAGAAGAACCCCCCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGAAGAAG GGCGGTTTAGCACCCGCTACGGGAACCAAAACGGTAGGATCCGGGTCCTGCAGAGGTTTG ACCAAAGGTCAAGGCAGTTTCAGAATCTCCAGAATCACCGTATTGTGCAGATCGAGGCCCA 643 GACCTAACACTCTTGTTCTTCCCAAGCACGCTGATGCTGATAACATCCTTGTTATCCAGC AAGGGCAAGCCACCGTGACCGTAGCAAATGGCAATAACAGAAAGAGCTTTAATCTTGACG AGGGCCATGCACTCAGAATCCCATCCGGTTTCATTTCCTACATCTTGAACCGCCATGACA AGGGCCATGCACTCAGAATCCCATCCGGTTTCATTTCCTACATCTTGAATCGACATGACA ACCAGAACCTCAGAGTAGCTAAAATCTCCATGCCCGTTAACACCCCGGCCAGTTTGAGG ATTTCTTCCCGGCGAGCAGCCGAGACCAATCATCCTACTTGCAGGGCTTCAGCAGGAATA 883 ATTTCTTCCCGGCGAGCAGCCGAGACCAATCATCCTACTTGCAGGATTCAGCAGGAATA CGTTGGAGGCCGCCTTCAATGCGGAATTCAATGAGATACGGAGGGTGCTGTTAGAAGAGA CTTTGGAGGCCGCCTTCAATGCGGAATTCAATGAGATACGGAGGCTGCTGCTTAGAAGAG ATGCAGGAGGTGAGCAAGAGGAAGAGGCCAGAGGCGATGGAGTACTCGGAGTAGTGAGA ACAATGAAGGAGTGATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACG 1060 ATAATGAAGGAGTGATAGTCAAAGTGTCAAAGGAGCACGTTCAAGAACTTACTAAGCACG CTAAATCCGTCTCAAAGAAAGGCTCCGAAGAAGAGGGGAGATATCACCAACCCAATCAACT TGAGAGGAGGCGAGCCCGATCTTTCTAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAG 1177 TGAGAGATGGCGAGCCCGATCTTTCTAACAACTTTGGGAGGTTATTTGAGGTGAAGCCAG ACAAGAAGAACCCCCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAG AAGGAGCTTTGATGCTCCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCGTCAACA AAGGAACTGGAAACCTTGAACTCGTGGCTGTAAGAAAAGAGGCAACAACAACAGGGGGACGGC AAGGAACTGGAAACCTTGAACTCGTAGCTGTAAGAAAAGAGCAACAACAGAGGGGGACGGC GGGAA-------GAAGAGGAGGACGAAGAAGAAGAAGAAGAGGGGAAGTAACAGAGAG 708 AACCTAACACTCTTGTTCTTCCCAAGCACGCTGATGCTGATAACATCCTTGTTATCCAGC 1297 463 (648 828 763 948 943 1068 1128 1188 1248 1308 1368 1428 1488 583 703 1008 403 168 888 891 528

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The invention relates to a modified anaphylactic food allergen whose amino acid sequence is substantially identical to that of a natural camphylactic food allergen. The natural anaphylactic food allergen is in a disulphide includes at least one cysteine residue that participates in a disulphide bond when the natural anaphylactic food allergen is in its native conformation, except that the cysteine residue has been modified anaphylactic food allergen, a nucleotide molecule of making a modified anaphylactic food allergen, a nucleotide molecule conformation a modified anaphylactic food allergen, a transgenic plant or nucleotide molecule for causing a site specific mutation in a gene conformation and modified anaphylactic food allergen defined above, a manimal expressing a modified anaphylactic food allergen defined above, a companylactic food allergen by administering a modified anaphylactic food allergen defined above, a natural anaphylactic food allergen by administering a modified or anaphylactic food allergen by administering a modified in at least or anaphylactic food allergen and is contacted with serum IgE from individual (s) allergen by an anaphylactic food allergen anaphylactic food allergen by adminimation and an isolated fragence or all the matural anaphylactic food allergen and IgE-binding epitopes of the English walnut allergen by an in Ara Distant and IgE-binding epitopes of the English and IgE-binding epitopes of the Engli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified anaphylactic food allergen comprising a cysteine residue which has been modified so that it cannot participate in the disulfide bond, useful for treating allergic reactions or wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAATGAGAGGGAGGTTTCTCCACTGATGCTTGTTGCTTGGGATCCTTGTCCTGGCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                  Sampson H, Bannon GA, Burks AW, Cockrell G;
on C, Helm RM, King NE, Kopper RA, Maleki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match

86.2%; Score 1750.8; DB 10; Length 1949;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 1893; Conservative 0; Mismatches 47; Indels 54; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1949 BP; 599 A; 456 C; 516 G; 378 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO 6; 194pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanley JS;
            02-MAR-1999; 99US-0122560P.
02-MAR-1999; 99US-0122565P.
02-MAR-1999; 99US-0122566P.
11-MAR-1999; 99US-00267719.
28-JAN-2000; 2000US-00494096.
16-MAR-2001; 2001US-0276822P.
                                                                                                                                                                                                                                                                                                                                                                                                                    Connaughton
                                                                                                                                                                                                               COCKRELL G.
COMPADRE C M.
CONNAUGHTON C.
                                                                                                                                                                                                                                                                                                                                                                                                                  Compadre CM, Connaugh
Rabjohn PA, Shin DS,
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KING N E.
KOPPER R A.
MALEKI S J.
RABJOHN P A.
SHIN D S.
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                                                                                                                                              SOSIN H B.
SAMPSON H.
BANNON G A.
BURKS A W.
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                                                                                                                                CAPLAN M J.
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(HELM/)
(KING/)
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(MALE/)
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                                                                                                                                                                                               AAGCGAAGGATTTAGCATTCCCTGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACC 1778
                                                                                                                                                                                                                                                                                                                                                                   -----GTCTCCTGAAAAGGGATCAAGAGGAGGAAAACCAAGGAGGAAGGGTC 1815
                                                                                                                                             CAGTAGCCATCAACGCTTCCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAA
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                                                                                                                                                                                                                                                                                                                                1839 CTGAGAAAGAGTCTCCTGAGAAAGAGGATCAAGAGGAGGAAAACCAAGGAGGGAAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peanut; plant; ss; gene; allergen; Ara hl; Ara h2; Ara h3; glycinin A2Bla; Jug n1; antiallergic; vulnerary; anaphylactic food allergen; IgE; allergy; wound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG27463 standard; cDNA; 1949 BP.
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96US-00712933.
98US-0073283P.
98US-0074624P.
98US-0074631P.
98US-0016872.
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99US-00240557.
99US-00241101.
99US-00248673.
99US-0122450P.
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23-SEP-1996;
31-JAN-1998;
13-FEB-1998;
13-FEB-1998;
29-JUN-1998;
27-AUG-1998;
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02-MAR-1999;
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TTTCTGCAACGCATGCCAAGTCATCACCTTACCAGAAAACAGAGAACCCCTGCGCCC		-ACACTG 222 SGAGACT 347 SGAGACT 282			CACCAGGTAGCCATGTGAGGAAGAACATCTCGGAACAACCCTTTCTACTTCCCGTCAA 587 [3AGGCCA 642 ATCCAGC 767 ATCCAGC 702	AAGGCAAGCCACCGTGACCGAATGCCAATAACAGAAAGGCTTTAATCTTGACG 827		ATTICTICCGGGGGGGCGGGGCCAATCATCTTGCAGGCTTCAGCAGGAATA 1007	GAAGAGA 1067 GAAGAGA 1002	AGTGAGA 1127 	1128 ACANTGAAGGAGTGATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACG 1187

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                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents anaphylactic antigen Ara h 1, cDNA clone P17. Ara h 1 is an anaphylactic antigen (A), which was used to design antigenic peptides having a reduced ability to bind immunoglobulin E (IEE) as compared with the inteact (A), or having a sequence substantially compared with the inteact (A), or having a sequence substantially compared by a portion of sequence of an antigen that includes at least one IEE binding site of the peptide is altered. The antigenic peptides are used in a composition which is useful for reducing risk or severity of allergic reaction to an antigen. This is done by identifying prior display of allergic symptoms when exposed to the antigen, or a familial relationship with an individual who compared with an antigen-specific IGE present on one or more mast cells or basophis in the individual's serum is identified. The individual is contacted with a peptide corresponding to a portion of the antigen, which is selected, formulated, and delivered as compared with IGE binding to entire and contact antigen. The composition is also useful for treating and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 ACGATGATGACCGCCGTCAACCCCGAAGAGGAGGAGGCCGATGGGGACCAGCTGGAC 407
                                                                                                                                                                                                                                                                                                                                   Antigenic fragments useful for reducing anaphylactic risk and reducing the severity and/or number of allergic symptoms in individuals sensitive to antigens, have reduced ability to bind Immunoglobulin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1952 BP; 608 A; 456 C; 512 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels
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                                                                                                                                                                                                                                                                       Sosin
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                                                                                                                                                                                                                                                                     Sampson H,
                                                                                                                                                                                                                 (UYAR-) UNIV ARKANSAS.
(MOUN ) MOUNT SINAI SCHOOL MEDICINE NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.1%; Score 1749.8; Best Local Similarity 95.0%; Pred. No. 0; Matches 1893; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 9; 100pp; English
                                                                                                                                                                                                                                                                       Caplan MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing allergic reactions
                                                                                                                                99US-00455294
2000US-0213765P
                                                                                                                                                                 2000US-0235797P
                                                                                              06-DEC-2000; 2000WO-US033124
                                                                                                                                                                                                    PANACEA PHARM LLC
                                                                                                                                                                                                                                                                     Burks WA,
                                                                                                                                                                                                                                                                                                     WPI; 2001-381378/40.
                               WO200140264-A2
                                                                                                                                                                 27-SEP-2000;
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23-JUN-2000;
                                                                 07-JUN-2001
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This invention relates to a novel isolated nucleic acid molecule encoding the peanut allergen Ara h I that has been identified in patients with a topic dermatritis. Specifically, it refers to a monoclonal antibody catopic dermatritis. Specifically, it refers to a monoclonal antibody catopic dermatritis. Specifically, it refers to a monoclonal antibody catopic and guantify the peanut allergens, where the monoclonal antibodies have specificity for a selected peanut allergen antigen. The present invention also describes by hybridomas that produce two-site monoclonal antibodies specific for a peanut allergen that can be used in an ELISA to detect and determine the concentration of a specific peanut allergen in a food product or in food produce or in food concentration of a specific peanut allergen or expression vector and the isolated nucleic acid or its fraction can include a diagnostic label. Accordingly, these nucleic acids are useful for obtaining diagnostics with optimal concentrations of each allergen or for developing panels of mixtures of large numbers of recombinant allergens such that it can be used in immunotherapy for the treatment of food hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGCCTTCAATGCGGAATTCAATGAGATAC 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reactions. This polynucleotide sequence is the peanut Ara h I allergen CDNA (clone 5 Ala) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGCCTTCAATGCGGAATTCAATGAGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              687 GTATTGTGCAGATCGAGGCCAAACCTAACACTCTTGTTCTTCCCAAGCACGCTGATGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747 ATAACATCCTTGTTATCCAGCAAGGCCAAGCCACCGTGACCGTAGCAAATGGCAATAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAAGAGCTTTAATCTTGACGAGGGCCATGCACTCAGAATCCCATCCGGTTTCATTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATCTTGAACCGCCATGACAACCAGAACCTCAGAGTAGCTAAAAATCTCCATGCCCGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACACACCCGGCCAGTTTGAGGATTTCTTCCCGGCGAGCCGAGCCGAGACCAATCATCCTACT
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                                                                                                                     New isolated nucleic acid encoding peanut allergen Ara h 1, useful fobtaining diagnostics with optimal concentrations of each allergen, developing panels of mixtures of recombinant allergens, and in
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                                   Helm
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Pred. No. 0;
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                                   Cockrell G,
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                                                                                                                                                                                                                 Disclosure; Col 75-78; 141pp; English
                                   Bannon GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.6%;
Matches 1340; Conservative
                                   Stanley JS,
(UYAR-) UNIV ARKANSAS
                                                                      2005-045982/05
                                                                                         P-PSDB; ADV97604
                                                                                                                                                                               immunotherapy
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                                     Burks AW,
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                                                                                                                                                                                                1538 AGTAGCCATCAACGCTTCCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAAA 1597
                                                                                                                                                                                                                                                    CAACCACAGAATCTTCCTTGCAGGTGATAAGGACAATGTGATAGACCAGATAGAGAAGCA 1719
                                                                                                                                                                                                                                                                           AGCGAAGGATTTAGCATTCCCTGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCA 1779
                                                                                                                                                                                                                                                                                                                                                1658 AGCGAAGGATTTAGCATTCCCCTGGTTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCA 1717
                                                                                                                                                                                                                                                                                                                                                                                                1780 GAAGGAATCTCACTTTGTGAGTGCTCGTCCTCAATCTCAATCTCCAATCTCCGTCGTCTCT 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1840 TGAGAAAGAGTCTCCTGAGAAAGAGGATCAAGAGGAGGAAACCAAGGAGGGAAGGGTCC 1899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allergen; atopic dermatitis; diagnostic; immunotherapy; immediate type hypersensitivity; Ara h I; dermatological; antiallergic; immunosuppressive; antibody engineering; gene; ss.
                                                                                                                                                                               AGTAGCCATCAACGCTTCCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAAA
                                                                                                                                            1478 GCGTAGGTACACAGCGAGGTTGAAGGAGGCGATGTGTTCATCATGATGCAGCAGCAGCTCATCC
   1358 AAGGAACTGGAAACCTTGAACTCGTAGCTGTAAGAAAAGAGCAACAACAGAGGGGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1900 ACTCCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTGTTATGTATCGATA
                                                             GGGAA-----GAAGAGGAGGACGAAGACGAAGAAGAGGGGGGAAGTAACAGAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Ara h 1 (clone 5 Ala) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                     Peanut Ara h I allergen alpha (clone 5 Ala) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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96US-00717933.
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23-SEP-1996;
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(Soybean) var. Wasesuzunari

/partial /product= "Glycine max protein #2"

Location/Qualifiers 1. .1251

1. .../ /*tag=

'note= "This sequence lacks a stop codon"

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21-DEC-2000; 2000JP-00405097
                                                                                                        21-DEC-2000; 2000JP-00405097
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               ATATCACCAAACCCAATCAACTTGAGAGAGAGCGAGCCCGGATCTTTCTAACAACTTTGGGA
                                                                          CAGCAGCTCATCCAGCCATCAACGCTTCCTCCGAACTCCATCTGCTTGGCTTCGGTA
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                                                                                                                                                                                                                                                                                                                              CTCCGTCGTCTCTCTGAGAAAGAGTCTCTGAGAAAGGGATCAAGAGGAGGAAAACCAAG
       ATATCACCAACCCAATCAACTTGAGAAGGCGAGCCCGATCTTTCTAACAACTTTGGGA
                                    AGTTATTTGAGGTGAAGCCAGACAAGAAGAACCCCCCAGCTTCAGGACCTGGACATGATGC
                                             TGGTTATCGTCGTCGTCACAAAGGAACTGGAAACCTTGAACTCGTGGCTGTAAGAAAG
                                                                                                                              TCAACGCTGAAAACAACCACAGAATCTTCCTTGCAGGTGATAAGGACAATGTGATAGACC
                                                                                                                                                                                                                                                                 AGATAGAGAAGCGAAGCGAAGGATTTAGCATTCCCTGGGTCGGCTGAACAAGTTGAGAAGC
                                                                                                                                                                                                                                                                                      TCATCAAAAACCAGAAGGAATCTCACTTTGTGAGTGCTCGTCCTCAATCTCAAT
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979 ATCCTACTTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGCCTTCAATGCGGAATTCAA 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new Glycinin characterised by the atomic coordinate data fully defined in the specification. The structure can be used for improving processability of soya protein. The present nucleic acid sequence encodes the Glycine max (Soybean) var. Wasesuzunari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                             Glycinin, beta-conglycinin and proglycinin, their crystal structures, three dimensional coordinates, three dimensional structured and models
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 AGACTACCGGATTGTCCAGTTTCAGTCAAAACCCAACACACAATCTTCTCCCCCACCATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1251 BP; 385 A; 304 C; 265 G; 297 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 62.2%; Pred. No. 1.3e-109; Matches 780; Conservative 0; Mismaranara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein #2, as described in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 1282-1283; 1298pp; Japanese.
                                                                                                                   WPI; 2002-685438/74
(KYOU ) UNIV KYOTO
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                                                                                                                                                                                                                                                                                                                                                         three dimension
and their uses.
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protein;

Soybean, Glycinin, atomic coordinate data, processability, soya Wasesuzunari, protein co-ordinate data, gene, ds. (Soybean) var. Wasesuzunari gene #2.

вР

DNA; 1251

standard;

ABS55196

ABS55196;

(first entry)

17-DEC-2002

пах

Glycine

max

Glycine

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Search completed: June 22, 2006, 11:35:24 Job time: 914.436 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

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EST608807

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EST635919

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EST636045 EST531298 EST636119 EST608029

EST610416

EST635688

Run on:

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Arachis hypogaea (peanut)

Kachis hypogaea

Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;

Aeschynomeneae; Arachis.

I (bases I to 721)

Struc, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.

and Lynch, R.E.

Generation and Analyses of ESTs for Arachis hypogaea

Unpublished (2003)

Contact: Bacatu Guo

Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd., Tifton, GA 31794, USA

Tel: 229-387-2334

Fax: 229-387-2321
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   June 23, 2006, 09:32:31 ; Search time 10443.4 Seconds (without alignments) 10880.347 Million cell updates/sec
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                GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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G 721

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(NOTEP) (NOTE = "Wector: Uni-ZAP XR, Site 1: ECORI; Site 2: Xhol, CDNA library was constructed from peanut cultivar Al3 (NCVIIXARA). Al3 has resistance to Appergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluesoript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                                                                                                                                                             Arachis hypogaea
Mekaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids 1, Pabales, Fabaceae, Papilionoideae,
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(UTPP)"
                                                                          Pod cDNA Library (UTPP) 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 714)
Luo, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.
and Lynch, R.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
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99.9%; Pred. No. 3.1e-189;
iive 0; Mismatches 1;
                                                                             UTPPI005_A03 USDA-Tifton Peanut Immature
Arachis_hypogaea cDNA clone UTPPI005_A03
                                                      mRNA
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/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPP1005_A03"
/tissue_type="Immature pods"
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/lab_host="XL1-blue"
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             GAAGGAGAACAAGAGTGGGGAACACCAGGTAGCCATGTGAGGAAGAAACATCTCGGAAC 420
TATGATCCTCGAGGACACACTGGCACCACCAACCAACGTTCCCCTCCAGGGGAGGGGACA 325
                                                                                     Arachis hypogaea (peanut)
Arachis hypogaea
Busaryota, Viridiplantaea, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids 1, Pabales, Fabaceae, Papilionoideae,
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Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                             ATCCGGGTCCTGCAGAGGTTTGACCAAAGGTCAAGGCAGTTTCAGAATCTCCAGAATCAC
                                                       AACCCTTTCTACTTCCCGTCAAGGCGGTTTAGCACCGCTACGGGAACCAAAACGGTAGG
                                                                                                                                                                                                                                                                                                                                                            ATCCGGGTCCTGCAGAGGTTTGACCAAAGGTCAAGGCAGTTTCAGAATCTCCAGAATCAC
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                                                                                                              GGCCGATGGGGACCAGCTGGACCGAGGGAGCGTGAAAGAGAAGAAGACTGGAGACAACCA
                                                                                                                                                                          GAAGGAGAACAAGAGTGGGGAACACCAGGTAGCCATGTGAGGGAAGAACATCTCGGAAC
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Molecular Genetics
WDBA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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1 (bases 1 to 723)
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//OTCE="Vector: Uni-ZAP XR; Site 1: ECORI; Site 2: Xhol; CDNA library was constructed from peanut cultivar A13 (NCV1XAR4). A13 has resistence to Appergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -800C freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 50bbp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise plauescript phagemids from the Uni-ZAP XR vector; and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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/cultivar="A13"
/db xref="taxon:3818"
/clone="UTPPIO08_E12"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_hoste="Xil-blue"
/clone lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
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Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
Wolecular Genetics
12747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
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                                                                                                                                                                                                                                                                    CD038837 17-Dp mRNA linear EST 07-MAY-2003 UTPPI012 H04 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPPI012_H04 5', mRNA sequence.
TCAATCTCAATCTCCAATCTCCGTCGTCTCCTGAGAAGAGTCTCCTGAGAAAGAGGATCA 1869
                                 TCAATCTCAATCTCAATCTCCGTCGTCTCCTGAGAAGAGTCTCCTGAGAAAGAGAGATCN 660
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Wataryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
rosida; eurosida I, Pabales, Fabaceae; Papilionoideae,
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(bases 1 to 717)
Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
Tel: 229-387-2334
Fax: 229-387-2321
                                                                                              AGAGGAGGAAAACCAAGGAGGGAAGGGTCCACTCCTTTCAATTTTGAAGGCTTTTA 1925
                                                                                                                             Gaps
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/lab_host="XL1-blue"
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/OCCE="Vector: Uni-ZAP XR; Site_1: ECORI; Site_2: Xhol; CDNA library was constructed from peanut cultivar Al3 (NCV11XAR4). Al3 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -800C freezer. Total RNA was isolated with TRIZOL-Reagent Ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Fromega). CDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using Xhol ECORI sites adapters. The lamda library was packed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UJUJ8172 T19 bp mRNA linear EST 07-MAY-2003 UTPP1003 D10 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPP1003_D10 5', mRNA sequence.
                                                                                                                                                                                                                                                                          Arachis hypogaea Eukaryota, Embryophyta; Tracheophyta; Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.

1 (bases 1 to 719)

1 (bases 1 to 719)
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                                                                                                       criricegaegritatricagergaagccagacaagaagaagccccagcritcaggaccrega
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USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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/lab_host="XL1_blue"
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CD038172
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                                                                                                                                                                                                                                                                        /dev_stāge="R6"
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/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPp)"
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                                                                                                                       /organism="Arachis hypogaea"
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                                                                           Location/Qualifiers
                            bguo@tifton.usda.gov
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Fax: 229-387-2321
                         Email: bguo@tif:
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                                                                                                                               GAGGGAGATATCACCAACCCAATCAACTTGAGAAGGCGAGCCCGATCTTTCTAACAAC 1279
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phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript hagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                  Length 719;
                                                                                 ; DB 4; Length 7 .4e-165; es 16; Indels
                                                                                 Score 629.2; D
Pred. No. 1.4e-
0; Mismatches
                                                                                 Query Match
Best Local Similarity 95.6%;
Matches 693; Conservative
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CD038790 676 bp mRNA linear EST 07-MAY-2003 UTPPI012_C06 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPPI012_C06 5', mRNA sequence.

CD038790.1 GI:30420628 EST. Arachis hypogaea (peanut)

CD038790

ACCESSION VERSION KEYWORDS SOURCE

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(UTPP) (U
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Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                    1 (bases 1 to 676)
Luo, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGCACTCAGAATCCCATCCGGTTTCATTTCCTACATCTTGAACCGCCATGACNACCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                Contact: Baozhu Guo
Molecular Genetics
WDBA/RS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2221
Email: bguo@tifton.usda.gov
                                                                                                                                                                                                                                                                               and Lynch, R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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es 670; Conserv
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and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -800C freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECRI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                             29.6%; Score 602; DB 4; Length 685; 94.3%; Pred. No. 6.6e-158; ive 0; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                               AAGAACCCCCAGCTTCAGGACCTGGACATGATGCTCA-CCTGTGTAGAGATCAAAGAGG 1371
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Arachis hypogaea
Bukaryora, Viridiplantaea, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
      GAGGTGAGCAAGAGGAGAGAGGCCAGAGGCCGATGGAGTACTCGGAGTAGTGAGAACAATG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
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1 (bases 1 to 685)

Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
and Lynch,R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
                                                                                                                                                                                                                                                                                                                     AGCTTTGATGCTCCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCGTCAACAAAGG
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                                                                                                                            CCGTCTCAAAGAAAGGCTCCGAAGAAGAGGGAGATATCACCAAACCAATCAACTTGAGAG
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/dev_stage="R6"
/lab_host="XL1-blue"

    . 685
    /organism="Arachis hypogaea"

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/clone="UTPP1009_A05"
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Email: bguo@tifton.usda.gov
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/cultivar="A13"
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567 522 627

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/db_xref="taxon:3818"
/clone="uTPP1008 G09"
/tissue_tvpp="Immature pods"
/dev_stage="R6"
/lab_nost="XL1-blue"
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/cultivar="A13"
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CD038119 588 bp mRNA linear EST 07-MAY-2003 UTPP1002 F11 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPP1002_F11 5', mRNA sequence.
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/lab_host="XLJ-blue"
/clone lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
                                                                                                                                                                                                                                                                             Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
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                                                                                                                                                                                                                                                                                                                   Generation and Analyses of ESTs for Arachis hypogaea Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit 219, Davis Rd, Tifton, GA 31794, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 28.3%; Score 576; DB 4; Length 588; al Similarity 99.8%; Pred. No. 1.4e-150; 587; Conservative 0; Mismatches 0; Indels
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/clone="UTPPI002_F11"
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Email: bguo@tifton.usda.gov
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/cultivar="A13"
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1 (bases 1 to 588)
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Arachis hypogaea
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Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I: Rabales; Fabaceae; Papilionoideae;
Aschynomeneae; Arachis.

(bases 1 to 684)
Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
and Lynch,R.E.
Generation and Analyses of ESTs for Arachis hypogaea
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181 CTCCGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAAACAACCACAGAATCTTCCT
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Unpublished (2003)
Contact: Baczhu Guo
Molecular Benetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -800C freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRL) mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The limad library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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/OCCE="Vector: Uni-ZAP XR; Site_1: ECORI; Site_2: Xhol; CDNA library was constructed from peanut cultivar Al3 (NCVIIXARA) al3 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRL) mRNA was extracted and purified from total RNA (Promega). CDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to exise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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   Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.

1 (bases 1 to 474)

Luo, M., Dang, P., Guo B 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .739 CCTGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAGAAGGAATCTCACTTTGTG
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                                                                                                                                                                                     Luo,M., Dang, T. (1974)

Luo,M., Dang, T. (1974)

and Lynch, R.E.

and Lynch, R.E.

Generation and Analyses of ESTs for Arachis hypogaea

Unpublished (2003)

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Local Similarity 99.8%; Pred. No. 1.5e-121;
les 473; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Immature_pods"
/dev_stage="R6"
/lab_host="XL1-blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3818"
/clone="UTPP1010_H08"
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Arachis hypogaea (peanut)
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CD038694 HAVE DEATH THEORY TITEON PEANLY TO THEORY CONTROL OF THE POD CDNA LIBRARY (UTPP) Arachis Typogaea cDNA clone UTPPI010_H08 5', mRNA sequence. CD038694.1 GI:30420532

DEFINITION ACCESSION VERSION

RESULT 11 CD038694 us-10-728-051-1.rst

was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."	Query Match 23.2%; Score 471; DB 4; Length 582; Best Local Similarity 91.5%; Pred. No. 5.9e-121; Matches 552; Conservative 0; Mismatches 19; Indels 32; Gaps 4;	Oy 1398 CAAAGGCCATGGTTGTCGTCGTCAACAAAGGAACTTGGAACTTGAACTCGTGGCTG 1457 	Qy 1458 TAAGAAAAAGACCAACAACAGAGCAACGCGGGAAGAAGAGGAGGACGAAG 1508	1509 ACCAMONACOGGO ACCAMON
OY 1799 AGTGCTCGTCCTCAATCTCAATCTCCGTCGTCGTCTCCTGAGAAAGAGTCTCCTGAG 1858	OY 1859 AAAGAGGATCAAGAGGAAAACCAAGGAGGGAAGGGTCCACTTCTATTTTGAAG 1918 	OY 1919 GCTTTTAACTGAGAATGGAGGAACTTGTTATGTATCGATAATAAGATCACGCTTTTGTA 1978	QY 1979 CTCTACTATCCAAAAACTTATCAATAAAAAACGTTTGTGCGTTGTTTGT	RESULT 12 COD3820 CO03820 CO03

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/UDER="Vector: Uni-ZAP XR; Site 1: ECORI; Site 2: Xhol; CDNA library was constructed from peanut cultivar Al3 (NCV11XARA). Al3 has resistance to Appergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). CDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using Xhol ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
                                                                                                                                                                                                                                                                                                              CD038101 484 bp mRNA linear EST 07-MAY-2003 UTPP1002 E01 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPP1002_E01 5', mRNA sequence.
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   Eukaryor i Puridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Ascschynomeneae; Aracchis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="Immature pods"
/dev_stage="R6"
/dev_stage="R6"
/lab_host="XL1-blue"
/clone lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
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                                                                                                                                460 TTGTAATCTACTCAAAAACTTATCAATAAATAAAACGTTTGTGCGT 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
                                                                                                   1974 TIGIACICTACTATCCAAAACTTATCAATAAAAAACGTTTGTGCGT
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21.5%; Score 436; DB 4; I
Best Local Similarity 93.8%; Pred. No. 4.2e-111;
Matches 473; Conservative 0; Mismatches 10;
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/mol_type="mRNA"
/cultivar="A13"
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/clone="UTPP1002_E01"
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EST.
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JOURNAL
COMMENT
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CD038101
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CGAGGTTGAAGGAGGGGATGTGTTCATCATGCCAGCAGCTCATCCAGCCATCAACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
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Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2147 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@rifton.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.6%; Score 458.8; DB 4; Length 509; Best Local Similarity 93.8%; Pred. No. 1.6e-117; Matches 497; Conservative 0; Mismatches 12; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UTPP1004_F03"
/tissue_type="Immature pods"
                                                                                                                                                                                                                                                                                       organism="Arachis hypogaea"
                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:3818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="R6"
/lab_host="XL1-blue"
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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                                                                                                                                                                                             Seg primer: T3
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Job time: 10446.4 secs
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                  Query Match 21.1%;
Best Local Similarity 98.0%;
Matches 434; Conservative
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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Yan, Y.S., Wang, L., Zhong, Y.J. and Huang, S.Z.
Yan, Y.S., Wang, L., Zhong, Y.J. and Huang, S.Z.
Expressed sequence tags of mid-matured cotyledons of peanut Unpublished (2004)
Contact: ShangZhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology GuangZhou, 510275, China
Tel: (860)02084036592
Email: yys980389ahoo.com.cn
Seq primer: pTriplExz Porward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      242 TCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAGAGGGAGTCTCACTTTGTGAGTGCT
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                                                              GAAGGCGATGTGTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCTCCGAA
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/dev_stage="Mid-matured stage"
/lab_host="E.coli BM25.8"
/clone_lib="Peanut Lambda Express library"
/note="Organ: Seed; Vector: lambdaTriplEx2"
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/cultivar="Yueyou 523"
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Arachis hypogaea
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AUTHORS
TITLE
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Length 443;
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Sequence 84,
Sequence 88,
Sequence 90,
Sequence 15,
Sequence 13,
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Sequence 4,
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                                                                                                          June 23, 2006, 09:43:18 ; Search time 316.712 Seconds
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
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US-09-106-872A-19

US-09-106-872A-19

US-09-106-872A-19

US-09-106-872A-19

US-09-106-872A-18

US-10-245-227D-84

US-10-245-227D-15

US-10-245-227D-15

US-10-245-227D-13

US-09-758-652-1

US-10-684-651-3

US-10-684-651-1

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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	ALIGNMENTS						
Seguence 11, Appl	US-10-235-618B-11	m	1318	2.1	43.4	45	
1, 4	-10-235-618B-1	m	1318	2.1	•	44	
17	US-09-949-016-17361	m	767677	2.5	43.8	43	
12147,	US-09-949-016-12147	m	767677	2.5	43.8	42	
13308,	US-09-949-016-13308	m	61664	2.5	44.2	41	
Sequence 16, Appl	US-10-235-618B-16	m	499	2.5	44.4	40	
	US-09-949-016-13632	m	300402	2.3	45.8		O
Sequence 7, Appli	US-09-323-195A-7	ო	1590	2.3	46	38	
	US-09-949-016-17388	m	74177	2.3	46.6	37	
	US-09-949-016-11988	٣	74177	2.3	46.6	36	
	US-09-710-794-3	ო	1068	2.4	49.4	35	
	US-08-232-463-14	~	7218	3.5	71.6		O
Sequence 1, Appli	US-10-264-303-1	٣		4.4	88.4	33	
	US-10-264-303-2	٣	1580	4.4	88.4	32	
	US-09-424-283-5	m	1924	4.9	98.8	31	
	US-07-955-905A-1	~	1867	6.8	138.8	30	
	US-10-684-651-2	m	1920	16.0	324.2	58	
	US-09-758-652-2	m	1920	16.0	324.2	28	
	US-09-108-010B-2	ო	1920	16.0	324.2	27	
Sequence 87, Appl	US-10-245-227D-87	m	1350	16.8	340.6	56	
Sequence 96, Appl	10-245-227D-	m	3808	19.8	402	25	
	US-10-245-227D-94	ო	3808	19.8	402	24	

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                                                                                    APPLICANT: Burks Jr., A. Wesley
APPLICANT: Stanley, J. Steven
APPLICANT: Stanley, J. Steven
APPLICANT: Cockrell, Gael
APPLICANT: King, Nina E.
APPLICANT: Sampson, Hugh A.
APPLICANT: Bannon, Hugh A.
APPLICANT: Bannon, Gary A.
TITLE OF INVENTION: Peanut Allergens and Methods
FILLE REFERENCE: HS 103 CIP
CURRENT APPLICANTON NUMBER: US/09/106,872A
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: PCT/US96/15222
PRIOR APPLICATION NUMBER: 1996-09-23
NUMBER OF SEO ID NOS: 23
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100.0%; Pred. No. 0;
live 0; Mismatches
                   Sequence 21, Application US/09106872A Patent No. 6486311 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Arachis hypogaea
US-09-106-872A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 2032; Conservative
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US-09-106-872A-21
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Mon Jun 26 09:18:35 2006

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	05 1621 CGAGTTCCATCTGCTTGGCTTTCGGTATCAAN 1681 AGGTGATAAGGACAATGTGATAGACCAGATP 1681 AGGTGATAAGGACAATGTGATAGACCAGATP 1741 TGGGTCGGGTGAACAAGTTGAGAAGCTCATC 1741 TGGGTCGGGTGAACAAGTTGAGAAGCTCATC 1741 TGGGTCGGGTGAACAAGTTGAGAAGCTCATC 1741 TGGGTCGGGTGAACAAGTTCAATCTCCATC 1801 TGCTCGTCCTCAATCTCAATCTCAATCTCCATC 181 TGCTGTCGTCCTCAATCTCAATCTCAATCTCCA 181 AGAGGATCAAGGAGGAAACCCAAGGAGGC 1821 TTTTAACTGAGAATGGAGGCAACTTGTTATC 1821 TTTTAACTGAGAATGGAGGCAACTTGTTATC 1821 TTTTAACTGAGAATGGAGGCAACTTGTTATC 1821 TTTTAACTGAGAATGGAGGCAACTTGTTATC 1821 TTTTAACTGAGAAACTTATCAATAAAAAAAAAAAAAAAA	RESULT 2 US-09-191-593-5 US-09-191-593-5 Sequence 5, Application US/09191593 Patent No. 6835824 Sequence 5, Application US/09191593 Patent No. 6835824 APPLICANT: BURKS, A Wesley, HELM, Ricki APPLICANT: BURKS, A Wesley, HELM, Ricki APPLICANT: BURNON, Garly A TITLE OF INVENTION: PERNUT ALLERGENS AN TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 67 CONTRESPONDENCE ADDRESS: ADDRESSE: Head, Johnson & Rachigian STREET: 112 W. Center St., Suite 230 STREET: ALW Center St., Suite 230 COUNTY: Fayetteville STATE: Arkansas AR COUNTY: Fayetteville STATE: Arkansas AR COMPUTER: BEADABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.6 MEDIUM TYPE: Storage COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Wordperfect 6.0C CURRENT APPLICATION DATA:
	1 GEGETACGGGAACCAACCCTTTCTACTTCCCGTCAAGGCGGTTTAGCC 600 601 CCGCTACGGGAACCACCCTTTCTACTTCCCGTCAAGGCGGTTTAGCCC 600 601 CCGCTACGGGAACCACACCCTTTCTACTTCCCGTCAAGGCGGTTTAGCCC 600 601 CCGCTACGGGAACCAAAACGGTAGGATCCGGGTCCTGCAGGGTTTGACCAAGGTCAAG 600 601 CCGCTACGGGAACCCAAAACGGTATCTGCAGAGGTTTGACCAAAGGTCAAG 600 601 CCGCTACGGGAACCCAAAACGGTATTGTGCAGAGGTTTGACCAAACCTCT 720 601 GCAGTTTCAGAATCTCCAGAATCACCGTATTGTGCAGAGGCCAAACCTAACACTCT 720 721 TGTTCTTCCCAAGCACGCTGATAACATACATCTTGTTATCCAGCAAGCCAACCCAC 780 721 TGTTCTTCCCAAGCACGCTGATAACATACATCTTTTATCCAGCAAGGCCAAGCCAC 780 721 TGTTCTTCCCAAGCAATACAAAAACAGAAACACTTTATCTGACGCAAGCCCATCCCT 720 721 TGTTCTTCCCAAGCAAAACGCTGATAACATCTTTATCTGACGCAAGCCCATCACT 780 722 TGTTCTTCCCAAGCAAAACACAAAAAAACACTTTAATCTTGACGAGGCCCATCCAC 780 723 TGTTCTTCCCAAGCAAAAACAAAAAAAAACCTTTAATCTTGACGAGGCCCATCACT 780 724 TGTTCTTCCCAAGCCAATAACAAAAAAACCTTTAATCTTGACGAGGCCCATCACT 780 725 TGTTCTTCCCAAGCCAATAACAAAAAAACCTTTAATCTTGACGAGGCCCATCACT 780 781 CGTGACCCTACCCGGTTTAACATCTTGAACACCAGAACCTCAG 900 781 CAGAATCCCATCCAATACCACCTTGAACCGCCATGACAACCTCAG 900 781 CAGAATCCCATCCAATAACAAAAAAACCTTTGAACACACGCCATGACAACCCAGGACCTCAG 900 781 CAGAATCCCATCCAATAACAAAACACACCCGCCATTTAAACATGACAAACCCAGGACCCTCAG 900 781 CAGAATCCCATCCAATACCACCCTTAAAAACTTTGAACAAAACCAAGAAACCCCAGCCCATTTAAACACAACACACCCCAAGAACCCAGGAACCTCCAGGCCATTAAAAATCTTCCAAAAATCCCATCAAAAATCCCATTAAAAATCTTTCCTAACACCCCCC	961 GAGCAGCCGAGACCATCATCTACTTGCAGGCTTCAGCAGGAATACGTTGGAGGCCGC 1020 961 GAGCAGCCGAGACCATCATCATACTTGCAGGCTTCAGCAGAATACGTTGGAGGCCGC 1020 961 GAGCAGCCGAGACCATCATCATCATCACTGCAGGAATACGTTGGAGGCCGC 1020 1021 CTTCAATGCGGAATTCAATGAGAACGGGCTGCTTAGAAGAATGCAGGAGGTGA 1080 1022 CTTCAATGCGGAATTCAATGAGAACGGGCTGCTTAGAAGAATGCAGGAGGTGA 1080 1024 CTTCAATGCGGAATTCAATGAGAACGGGCTGCTTAGAAGAAATGCAGGAGGTGA 1080 1081 GCAAGAGGAGAGGGGAGAGGCGATGGAGTACTTAGAAGAAATGCAGGAGTTA 1140 1141 GATAGTCAAAGTGCAAAGGAGCGATGGAGTACTTAGAAGAAATGAAGGAGT 1140 1141 GATAGTCAAAGTGCAAAGGAGCAGTTGAAAACTTAGAAAACAGAAGTT 1200 1141 GATAGTCAAAGTGCAAAAGAGGAGCACTTAACTAAGCACCTAAATCCGTCT 1200 1141 GATAGTCAAAGTGCAAAAGAGGAGAATTACTAAGCACGCTAAATCCGTCT 1200 1201 AAAGAAAGGTCCAAAAAGAGAGAAATTACTAAAAAAGAAAAGAGAAGAAGAAATGAAAAAGTGCTTTAGGAAAAAGAAATTATCACCAACCCAATCAAAAAAGAAAAGAAAAAAAA
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JATION METHOD: By agreement with IDENTIFICATION METHOD: protein information and established IDENTIFICATION METHOD: consensus sequence OTHER INFORMATION: allergen Protein and FULLCATION INFORMATION: allergen TITLE: JOURNAL: VOLUME: ISSUE: PAGES: DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE: P41b
POSITION IN GENOME:
CHROMOSOME/SEGMENT: No. 6835824 applicable
NAP POSITION: No. 6835824 applicable
NAP POSITION: No. 6835824 applicable
NATCS: No. 6835824 applicable
FATURE:
NAME/KEY: CDS
LOCATION: 50..1930
IDENTIFICATION METHOD: By agreement with
IDENTIFICATION METHOD: consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA DESCRIPTION: identified as Ara h I Beta P41b HYPOTHETICAL: No
PILING DATE: 13 NOVEMBER 1998
CLASSIFICATION:
PRIOR APPLICATION DATA: 48
APPLICATION NUMBER: 08/717,933
FILING DATE: 23 SEPTEMBER 1996
APPLICATION NUMBER: US 07/998,377
FILING DATE: 29 NOVEMBER 1992
APPLICATION NUMBER: US 08/158,704
FILING DATE: 29 NOVEMBER 1993
APPLICATION NUMBER: US 08/10,424
FILING DATE: 29 DECEMBER 1995
APPLICATION NUMBER: US 08/610,424
FILING DATE: 04 MARCH 1996
ATTORNEY AGENT INFORMATION:
NAME: ALEXANDER, DANIEL R
REGISTRATION NUMBER: 32,604
REFERENCE/DOCKET NUMBER: ARKO0895601B
TELLEPHONE: (501) 521-4931
TELLEPHONE: LENGRAL APPLICABLE
SEQUENCE CHARACTERISTICS:
LENGRH: 2032 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: Florunner seed cDNA expression
LIBRARY: library in Uni-ZAP XR vector
CLONE: P41b
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DEVELOPMENTAL STAGE: Seed
HAPLOTYPE: No. 6835824 applicable
TISSUE TYPE: Seed mRNA, cDNA library
CELL TYPE: No. 6835824 applicable
CELL LINE: No. 6835824 applicable
ORGANELLE: No. 6835824 applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 6835824 applicable
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-191-593-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: No FRAGMENT TYPE: No. 6835824 at ORIGINAL SOURCE: ORGANISM: Arachis hypogaea STRAIN: Florunner
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                AATAATCATATATATATTCATCCATCTATATAAGTAGTAGCAGGAGCAATGAGGAGGAG
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   Length 2032
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Query Match 100.0%; Score 2032; Best Local Similarity 100.0%; Pred. No. 0; Matches 2032; Conservative 0; Mismatches
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y dg	GATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACGCTAAATCCGTCTC	; FILE REFERENCE: 072121/0104 ; CURRENT APPLICATION WUMBER: US/09/715,036 ; CURRENT FILING DATE: 2000-11-20 ; PRIOR APPLICATION NUMBER: 60/167,255
oy Oy	1201 AAAGAAAGGCTCCGAAGAAGAGGGAGATATCACCAACCCAATCAACTTGAGAGAGGGGG 1260 	; PRIOR FILING DATE: 1999-11-19 ; NUMBER OF SEQ ID NOS: 8 ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 5
& a	1261 GCCCGATCTTTCTAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAGAACCC 1320 	; I.ENGTH: 2032 ; TYPE: DNA ; ORGANISM: Arachis hypogaea US-09-715-036-5
ò 8	1321 CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAGAAGGAGCTTTGAT 1380 	Query Match 100.0%; Score 2032; DB 3; Length 2032; Best Local Similarity 100.0%; Pred. No. 0; Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
os da	1381 GCTCCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCGTCAACAAGGAACTGGAAA 1440 	Oy 1 AATAATCATATATTCATCAATCATCTATATAAGTAGTAGGAGCAATGAGAGGAG 60
رن م	1441 CCTTGAACTCGTGGCTGTAAGAAAAGAGCAACAACAAGAGGGGGGGG	Qy 61 GGTTTCTCCACTGATGCTGGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA 120 Db 61 GGTTTCTCCACTGATGCTGGTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA 120
රු සි	1501 GGACGAAGACGAAGAGAGGAAGTAACAGAGAGGTGCGTAGGTACGTAC	Qy 121 TGCCAAGTCATCACCTTACCAGAAGAAAACAGAGAACCCCTGCGCCCCAGAGGTGCCTCCA 180 Db 121 TGCCAAGTCATCACCATACCAGAAGAAAACAGAGAACCCTGCGCCCAGAGGTGCCTCCA 180
දු පු	1561 GAAGGAAGGCGATGTGTTCATGAGGAGCTCATCCAGTAGCCATCAAGGCTTCCTC 1620 	Qy 181 GAGTTGTCAACAGGAACCGGATGACTTGAAGCAAAAGGCATGCGAGTCTCGCTGCACAA 240 Db 181 GAGTTGTCAACAGGAACCGGATGACCAAAAGGCATGCGAGTCTCGCTGCAA 240
% qa	1621 CGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAACAACCACAGAATCTTCCTTGC 1680 	Qy 241 GCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACACTGGCACCACCACCAACCA
\(\frac{4}{5} \)	1681 AGGTGATAAGGACAATGTGATAGACCAGATAGAGAAGCAAGC	Qy 301 ACGITCCCTCCAGGGAGCGGACACGCGCCCAACCCGGAGACTACGATGATGACGG 360
<i>상</i> 원	1741 TGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAGAAGGAATCTCACTTTGTGAG 1800 	Qy 361 CCGTCAACCCCGAAGAGGAAGCCCGATGGGGACCAGCTGGACCGAGGGGGGGA 420 bb 361 CCGTCAACCCCGAAGAGGAAGCCGATGGGGACCAGCTGGACCAGGGGGGGG
& d	1801 IGCICGICCICAAICICAAICICCATCICGICGICCICGAGAAAGAGICICCIGAGAA 1860 	Qy 421 AAGAGAAGAACTGGAGACAACAAGAGAAGATTGGAGGCCACCAAGTCATCAGCAGCC 480 421 AAGAGAAGAAGAACTGGAGAACACCAAGAAAAATTGGAGGCGACCAAGTCATCAGCAGCC 480
දු පු	1861 AGAGGATCAAGAGGAGAAAACCAAGGAGGGAAGGGTCCACTCCTTTCAATTTTGAAGGC 1920 	Qy 481 ACGGAAAATAAGGCCCGAAGGAAGAAGAAGAAGAAGAGAACACAGGTAGCCA 540 Db 481 ACGGAAAATAAGGCCCGAAGGAAGAAGAAGAAGAACAAGAGAACAAGAGAACACAGGTAGCCA 540
රු සි	1921 TTTTAACTGAGAATGGAGCAACTTGTTATGTATCGATAATAAGATCACGCTTTTGTACT 1980 	Oy 541 IGTGAGGGAAGAAACATCTCGGAACAACCCTTTCTACTTCCCGTCAAGGCGGTTTAGCAC 600 541 IGTGAGGGAAGAACATCTCGGAACAACCTTTCTACTTCCGTCAAGGCGGTTTAGCAC 600
γς do	1981 CTACTATCCAAAAACTTATCAATAAAAAGGTTTGTGCGTTGTTTCTCC 2032 	Qy 601 CCGCTACGGGAACCAAAACGGTAGGATCCTGCAGAGGTTTGACCAAAGGTCAAG 660
RESULT		
US-09-7 Seque Paten	US-09-715-036-8; Application US/09715036; Sequence 5, Application US/09715036; Patent No. 6943010; GENERAL INFORMATION:	

RESULT 3
US-09-715-036-5
Sequence 5, Application US/09715036
; Patent No. 6943010
; GENERAL INFORMATION:

721 TGTTCTTCCCAAGCACGCTGATGCTGATAACATCCTTGTTATCCAGCAAGGGCAAGCCAC 780

Oy 1861 AGAGGATCAAGAGAAAACCAAGGAGGAAGGGTCCACTCCTTTCAATTTTGAAGGC 1920	RESULT 4 US-09-106-872A-23 i Sequence 23, Application US/09106872A j Patent No. 6486311 j Patent No. 6486311 j APLICANT: Burke Jr., A. Wesley j APPLICANT: Sampson, Hugh A. APPLICANT: Sampson, Hugh A. APPLICANT: Bannon, Gary A. APPLICANT: Bannon, Gary A. APPLICANT: Bannon, Gary A. PETER OF INVENTION: Peanut Allergens and Methods FILE REFERENCE: H 103 CIP CURRENT APPLICATION NUMBER: US/09/106,872A CURRENT FILING DATE: 1999-06-29 PRIOR PLILING DATE: 1996-09-23 NUMBER OF SEQ ID NOS: 23 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 23 LENGTH: 2041 TYPE: DNA CURRANT Arachis hypogaea US-09-106-872A-23	QUESTY MATCH 100.0%; Score 2032; DB 3; Length 2041; Best Local Similarity 100.0%; Pred. No. 0; Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AATAATCATATATACATCATCATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60 Db 1 AATAATCATATATTCATCAATCATCATATAAGTAGTAGCAGGAGCAATGAGAGGGG 60 QY 61 GGTTTCTCCACTGATCATCATCTTGTTCTTCTTCTTCTTCTTCTTCTTCTAGTTTTTCTCAAGGGGG 60 Db 61 GGTTTCTCCACTGATCATTTGTTCTTCTTGTTCTTCTTCTTCTTCTTCTTCTTCTTC
DD 721 TGTTCTTCCCAAGCACGCTGATGCTGATAACATCCTTGTTATCCAGCAAGGGCAAGCCAC 780	CCGAGACCAATCATCCTACTTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGC GCGAGACCAATCATCCTACTTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGC GGGAGACCCAATCATCATTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGC GGGAGATTCAATGAGATACGAGGGTGCTGTTAGAAGAATGCAGGGGGA GGGAGAGGCGAATGAAGAATACGGAGGTGCTGTTAGAAGAATGCAGGAGGTGA GGGAGAGAGGCGATGGAGGTGCTGTTAGAAGAATGCAGGGGGA GGAGAGAGGGCGATGGAGGTGCTCGGAGTAGTGAAGAATGCAGGTGA GGAGAGAGGGCAGAGGATGAAGAACTTACTAGAAAACAATGAAGGAGT CAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACCCGTCTC CAAAGTGTCAAAGAAGGAGAATATCACCAATCACTAAATCCGTCTC CAAAGTGTCAAAGAAGAAGAATATTTGAGGTAAACTTAGAAAGAA	1321 CCAGCTTCAGGACCTGATAGTTCH

### #AGAGAGAGACACCAGAGAGACACCAGAGAGACACAGAGACAGAGACAGCAG	1501 GGACGAAGGAGGAAGGAAGGAAGTAACAGAGGGGGGTGCGTAGCTACACGCGAGGTT 1560	RESULT 5 Sequence 3, Application US/09106872A
		GAGCAGCCGAGATCATCATCCTACTTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGC GAGCAGCCGAGACCAATCATCCTACTTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGC CTTCAATGCGCGAATTCAATGCATCCTTGCAGGGCTGTTAGAAGAAATACGTTGGAGGCCGC CTTCAATGCGGAATTCAATGAGATACGGAGGGTGTTTAGAAGAAAAATCCTTGAGAGAGA

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1201 AAGAAAGGCTCCGAAGAAGAGGGAAGTATCACCAATCCAACTCAACTTGAGAGAAGGCGA 1260 121 CCCGATCTTTCTAACAACTTTGGGAAGTTATTGGGTGAAGCCGAACAAGAAGACCC 1220 122 CCAGCTTCAGGACTCAACTTTGGGAAGTTATTTGGGTGAAGCCAACAACAACAACAACACCAACAACAACAACAACA	RESULT 6 US-09-106-872A-19 Sequence 19, Application US/09106872A Sequence 19, Application US/09106872A Sequence 19, Application US/09106872A Sequence 19, Application Sequence 19, Nina E. Septicant: King, Nina E. Septicant: King, Nina E. Septicant: Halm, Ricki M. Septicant: Bannon, Gary A. Sequence 19, 100 Sequence 19, 100, 100, 100, 100, 100, 100, 100,
121 TGCCAAGTCATCACTTACCAGAAGAAACCAGAAACCCCTCGCCCCCAAGGGTGCCTCCA 180 121 TGCCAAGTCATCACCTTACCAGAAGAAAACCAGAAACCCCTCGCCCCCCCAAGGGTGCCCCCCA 180 121 TGCCAAGTCATCACCTTACCAGAAGAACACCAGAACCCCTCCCCCCCC	901 AGTAGCTAAAATCTCCATGCCCGTTAACACACCCGGCCAGTTTGAGGATTTCTTCCCGGC 960 901 AGTAGCTAAAATCTCCATGCCGGTTAACACACCCGGCCAGTTTGAGGATTTCTTCCCGGC 960 901 AGTAGCTAAATCTCCATGCCGGTTAACACACCCGGCCGGTTTGAGGATTTCTTCCCGGC 960 961 GAGCAGCCGAGACCAATCATTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGC 1020 1021 CTTCAATGCGGAATTCAATGAGATACGGAGGGTTTAGAAGAGAATGCTGGAGGCCGC 1020 1021 CTTCAATGCGGAATTCAATGAGATACGGAGGGTGTTTAGAAGAGAATGCAGGAGGTGA 1080 1021 CTTCAATGCGGAATTCAATGAGATACGGAGGGTGTTTAGAAGAAATGAAGGAGTA 1080 1081 GCAAGAGGAGAGGCGCAGGAGGGTACTCGGAGTAGTAGAAAAGGAGGTA 1140 1081 GCAAGAGGAGAGGCGAGGGGATGGAGGTACTCGGAGTAGTAGAAAAGGAGGTA 1140 1141 GATAGTCAAAGGAGGAGGCATGGAGTACTCGGAGTAGTAAAGGAGTT 1140 1141 GATAGTCAAAGGAGGAGGCATGAAACTTGAAGAACTTACTAAGCACTAAATCCGTCTC 1200 1141 GATAGTCAAAGGAGGAGGAGGATTGAAAACTTACTAAGCACGCTAAATCCGTCTC 1200 1101 GATAGTCAAAGGAGAGAGAGAGAATTACTAAGCACCTAAATCCGTCTC 1200 1101 GATAGTCAAAGGAGAGAGAGAGAATTACTAAGCACCTAAATCCGTCTC 1200 1101 GATAGTCAAAGGAGAGAGAGAGAATTACTAAGCACGCTAAATCCGTCTC 1200 1101 GATAGTCAAAGGAGAGAGAGAGAATTACTAAGCACGCTAAATCCGTCTC 1200 1101 GATAGTCAAAAGGAGAGAGAGAGAATTACTAAGCACGCTAAATCCGTCTC 1200 1101 GATAGTCAAAAGGAGAGAGAGAATTACTAAGCACCCAATCAAATCCGTCTC 1200

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AAGGACCTTTGATGCTCCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCGTCAACA
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CGTTGGAGGCCGCCTTCAATGCGGAATTCAATGAGATACGGAGGGTGCTGTTAGAAGAGA
         CTTTGGAGGCCGCCTTCAATGCGGAATTCAATGAGATACGGAGGGTGCTGTTAGAAGAGA
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                                       Query Match
Best Local Similarity 95.0%;
Matches 1894; Conservative
                 hypogaea
; LENCTH: 1949
; TYPE: DNA
; ORGANISM: Arachis
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APPLICANT: BARNAS, A Wesley, HELM, Ricki M, APPLICANT: COCKRELL, Gael, STANLEY, J Steven, APPLICANT: BANNON, Gary A TITLE OF INVENTION: PEANUT ALLERGENS AND TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 67 CORRESPONDENCE. ADDRESS: ADDRESSE: Head, Johnson & Kachigian STREET: 112 W. Center St., Suite 230 CITY: Payetteville STATE: Arkanasa AR CONNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 72701
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS. DOS 6.2
SOFTWARE: Wordperfect 6.0C
CURRENT APPLICATION DATA:
FILING DATE: I3 NOVEMBER 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: identified as Ara h I Alpha P17
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APPLICATION NUMBER: 08/117,933
FILING DATE: 23 SEPTEMBER 1996
APPLICATION NUMBER: 08 0/198,377
FILING DATE: 30 DECEMBER 1995
APPLICATION NUMBER: 08 08/158,704
FILING DATE: 29 NOVEMBER 1993
APPLICATION NUMBER: US 60/009,455
FILING DATE: 29 DECEMBER 1995
APPLICATION NUMBER: US 60/009,455
FILING DATE: 09 DECEMBER 1995
ATTORNEY/ACENT INFORMATION:
NAME: ALEXANDER, DANIEL R
REGISTRATION NUMBER: 32,604
REGISTRATION NUMBER: 32,604
TELEPRENCE/DOCKET NUMBER: ARK00895601B
TELEPAN: (501) 521-4931
TELEPAN: (501) 521-4931
TELEPAN: 1948 ASPLICABLE
INFORMATION FOR SEQ 1D NO: 4:
SEMENTIAL OF SECOND SECOND
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POSITION IN GENOME:
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DEVELOPMENTAL STAGE: Seed
HAPLOTYPE: No. 6835824 applicable
TISSUE TYPE: Seed mRNA, cDNA library
CELL TYPE: No. 6835824 applicable
CELL LINE: No. 6835824 applicable
ORGANELLE: No. 6835824 applicable
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ORIGINAL SOURCE:
Sequence 4, Application US/09191593
Patent No. 6835824
GENERAL INFORMATION:
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                                                     FEATURE:
NAME/KEY: CDS
LOCATION: 3..1847
LOENTIFICATION METHOD: By agreement with
IDENTIFICATION METHOD: protein information and established
IDENTIFICATION METHOD: consensus sequence
OTHER INFORMATION: Seed storage protein and
OTHER INFORMATION: allergen
PUBLICATION INFORMATION:
CHROWOSOME/SEGMENT: No. 6835824 applicable MAP POSITION: No. 6835824 applicable UNITS: No. 6835824 applicable
                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                           JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                                         AUTHORS:
TITLE:
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                                                                                                                                                                                                                                                                                             PAGES:
DATE:
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US-10-245-227D-88
Sequence 88, Application US/10245227D
Perent No. 6936696
GENERAL INFORMATION:
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Sequence 84, Application US/10245227D
GENERAL INFORMATION.
APPLICANT: Monsanto Company
APPLICANT: Rapp, William D.
APPLICANT: Peng, Jiexin
APPLICANT: Pong, Jiexin
APPLICANT: Peng, Jiexin
TITLE OF INVENTION: Enhanced Protein and Methods of The
FILE REFERENCE: REN-00-087 US
CURRENT APPLICATION NUMBER: US/10/245,227D
CURRENT APPLICATION NUMBER: US/10/245,227D
CURRENT FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATENTIN VEXSION 3.3
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Pred. No. 3e-113;
0; Mismatches 381;
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Local Similarity
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                                                                                                                                                                                                    2076 AAAGGCCATAGTGATACTAGTGATTAATGAAGGAGATGCAAACATTGAACTTGTTGGCAT
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APPLICANT: Rapp, William D.
APPLICANT: Peng, Jiein D.
APPLICANT: Peng, Jiein D.
APPLICANT: Nadig, Gautham
APPLICANT: Vaning Gautham
APPLICANT: Vankagondlu
TITLE OF INVENTION: Enhanced Protein and Methods of Their Use
FILE REFRENCE: REN. 00-087 US
CURRENT APPLICATION NUMBER: US/10/245,227D
CURRENT FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.3
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Pred. No. 6e-113;
0; Mismatches 381;
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; Patent No. 6936696
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Best Local Similarity 62.2
Matches 780; Conservative
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; LENGTH: 3808
; TYPE: DNA
; ORGANISM: Glycine max
US-10-245-227D-90
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US-10-245-227D-90
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                                                                                                                                                                        Their Use
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APPLICANT: Monsanto Company
APPLICANT: Rapp, William D.
APPLICANT: Rapp, William D.
APPLICANT: Nadig, dautham
APPLICANT: Nadig, Gautham
APPLICANT: Venkatesh, Tyamagondlu
TITLE OF INVENTION: Enhanced Protein and Methods of
FILE REFERENCE: REN-00-087 US
CURRENT APPLICATION NUMBER: US/10/245,227D
CURRENT FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.3
SEQ ID NO 88
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62.2%; Pred. No. 6e-11-,
1... 0; Mismatches 381;
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Matches 780; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: mature form of beta-conglycinin beta-subunit
US-10-245-227D-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1254;
                                                                                                                                                                  Protein and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.0%; Score 406.8; DB 3; Best Local Similarity 62.1%; Pred. No. 8.9e-113; Matches 779; Conservative 0; Mismatches 382;
                                                       APPLICANT: Monsanto Company
APPLICANT: Rapp, William D.
APPLICANT: Peng, Jiexin
APPLICANT: Peng, Jiexin
APPLICANT: Venkatesh, Tyamagondlu
TITLE OF INVENTION: Enhanced Protein and Methr
FILE REFERENCE: REN-00-087 US
CURRENT APPLICATION NUMBER: US/10/245,227D
CURRENT FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial
Sequence 15, Applicat
Patent No. 6936696
GENERAL INFORMATION:
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                                          CAATAACAGAAAGAGCTTTAAATCTTGACGAGGCCCATGCACTCAGAATCCCATCCGGTTT
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679 GAATCACCGTATTGTGCAGATCGAGGCCAAACCTAACACTCTTGTTCTTCCCAAGCACG 738 168 AGACTACCGGATTGTCCAGTTTCAGTCAAACCCAACACACAC	859 348	y 919 GCCGGTTAACACCCGGCCAGTTTGAGGATTTCTTCCCGGCGAGCGA	y 979 ATCCTACTIGCAGGGCTTCAGCAGGAATACGTIGGAGGCCGCCTTCAAIGGGAATTCAA 1038	y 1039 TGAGATACGGAGGTGCTGTTAGAAGAGAATGCAGGAGGTGAGCAAGAGAGAG	y 1099 GAGGCGATGGAGTACTCGGAGTAGTGACAACAATGAAGAGTGATGATAGTCAAAGTGTCAAA 1158	y 1159 GGAGCACGTTGAAGAACTTACTAAGCACGCTAAATCCGTCTCAAAGAAGGCTCCGAAGA 1218	y 1219 AGAGGGAGATATCACCAACCAATCAACTTGAGAAGGGGAGCCGGATCTTTCTAACAA 1278	y 1279 CTTTGGGAAGTTATTTGAGGTGAAGACAAGAAGAACCCCCAGCTTCAGGACCTGGA 1338	y 1339 CATGATGCTCACCTGTGTAGAGATCAAAGAAGGAGCTTTGATGCTCCCACACTTCAACTC 1398	y 1399 AAAGGCCATGGTTATCGTCGTCGACAAAGGAACTGGAAACCTTGAACTCGTGGCTGT 1458	y 1459 aagaaaagagcaacagaggaacggaggaagaagaagaaga	y 1519 GGAGGGAAGTAACAGAGGTGCGTAGGTACACAGGGAGGTTGAAGGAAG	y 1579 CATCATGCCAGCAGCTCATCAGTAGCCATCAACGCTTCCTCCGAACTCCATCTGCTTGG 1638	y 1639 CTTCGGTATCAACGCTGAAAACCACAGAATCTTCCTTGCAGGTGATAAGGACAATGT 1698	y 1699 GATAGACCAGATAGAGAAGCAAGGATTTAGCATTCCCTGGGTGAACAAGT 1758
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                                                                                      CACTTACTATTTGGTTAACCCTCACGACCACCAGAATCTCAAATAATCAAACTTGCCAT
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Pred. No. 9.2e-113;
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                                                                                                                                                                           APPLICANT: ANTHONY JOHN KINNEY
APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FABER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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APPLICATION NUMBER: US/09/108,010B
FILING DATE: 30-Jun-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROFSOFT WORD 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES OF AMERICA ZIP: 19898
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                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE
STREET: 1007 MARKET STREET
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                                                                                                                           Sequence 3, Application US/09108010B
Patent No. 6362399
GENERAL INFORMATION:
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TELEFAX: 302-773-0164
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
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62.1%;
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                                                                                   STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 406.8; DB 3;
Pred. No. 9.2e-113;
0; Mismatches 382;
            GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
                                                                                                                                                                                                                                           95
                                                                                                                                                                                                          MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROFOST WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/09/758,652
FILING DATE: 11-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-758-652-3
APPLICANT: ANTHONY JOHN KINNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.1%;
Matches 779; Conservative
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                                                                        NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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979 ATCCTACTTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGCCTTCAATGCGGAATTCAA
                               510 GTCCTACTTGCAAGGCTTCAGCCATAATATTCTAGAGACCTCCTTCCATAGCGAATTCGA
                                                                                                                                                                                                                               -----GGAGTGATCGTGGAACTCTCAAA
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                                                                                           219 AGAGGGAGATATCACCAACCCAATCAACTTGAGAGAAGGCGAGCCCGATCTTTCTAACAA
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                                                                                                                                                                                 .099 GAGGCGATGGAGTACTCGGAGTAGTGGAACAATGAAGGAGTGATAGTCAAAGTGTCAAA
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Search completed: June 23, 2006, 10:41:41 Job time : 326.712 secs

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1: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USO7_PUBCOMB.seq:*
2: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USO8_PUBCOMB.seq:*
3: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USO8_PUBCOMB.seq:*
4: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USO9B_PUBCOMB.seq:*
5: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USO9B_PUBCOMB.seq:*
6: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USO0C_PUBCOMB.seq:*
7: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USIOB_PUBCOMB.seq:*
8: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USIOB_PUBCOMB.seq:*
9: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USIOB_PUBCOMB.seq:*
10: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USIOF_PUBCOMB.seq:*
11: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USIOF_PUBCOMB.seq:*
12: / FBMC_Calerra_SIDS3/prodata/2/pubpna/USIOF_PUBCOMB.seq:*
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GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-72B-323-1

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US-10-99-551-1

US-10-99-551-1

US-10-98-324-5

US-10-98-324-5

US-10-100-303A-6

US-10-100-303A-6

US-10-100-303A-6

US-10-245-227B-13

US-10-75-27B-3

US-10-757-074-3

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Listing first 45 summaries
                                                                                                    nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Gaps

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Length 2032; Indels

DB 3; .; 0

Query Match
100.0%; Score 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches

LENGTH: 2032 TYPE: DNA ORGANISM: Arachis hypogaea

SEQ ID NO 1

US-09-731-375A-1

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GGTTTCTCCACTGATGCTGTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTTCTGCAACGCA 120

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61 GGTTTCTCCACTGATGCTGTTGCTAGGGATCCTTGTCCTGGCTTCAGTTTCTGCAACGCA

121 TGCCAAGTCATCACCTTACCAGAAGAAACAGAGAACCCTGCGCCCAGAGGTGCCTCCA 121 TGCCAAGTCATCACCTTACCAGAAGAAACAGAGAACCCCTGCGCCCAGAGGTGCCTCCA

1 AATAATCATATATATTCATCATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGGG

1 AATAATCATATATATCATCAATCATCTATATAAGTAGCAGGAGCAATGAGAGGGAG

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Sequence 1, Application US/10728323

Publication No. US20040208894A1

GENERAL INFORMATION:
APPLICANT: Caplan, Michael J.
APPLICANT: Bottomly H., Kim
APPLICANT: Bottomly H., Kim
APPLICANT: Sosin B., Howard
APPLICANT: Sampson A., Hugh
ITLE OF INVENTION: Microbial Delivery System
FILE OF INVENTION: Microbial Delivery System
CURRENT APPLICATION NUMBER: US/10/728,323

CURRENT APPLICATION NUMBER: 00/33-12-04

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 09/731,375

PRIOR PILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 1
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US-10-728-323-1
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Best Local Similarity 100.
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APPLICANT: Bottomly H., Kim
APPLICANT: Bottomly H., Kim
APPLICANT: Bottomly H., Kim
APPLICANT: Bottomly H., Kim
APPLICANT: Burks A., Wesley
APPLICANT: Sampson A., Hugh
TITLE OF INVENTION: Microbial Delivery System
FILE REFERENCE: 2002834 .022
CURRENT APPLICATION NUMBER: US/10/728,051
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: 60/195,035
PRIOR APPLICATION NUMBER: 09/731,375
PRIOR APPLICATION NUMBER: 09/731,375
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN POR: 2.1
SEQ ID NO S: 2.1
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100.0%; Pred. No. 0;
live 0; Mismatches
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; Publication No. US20040234548A1
; GENERAL INFORMATION:
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, ORGANISM: Arachis hypogaea
US-10-728-051-1
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Qy 1381 GCTCCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCGTCAACAAGGAACTTGGAAA 1440 Db 1381 GCTCCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCGTCAACAAGGAACTGGAAA 1440 Qy 1441 CCTTGAACTCGTGGCTGTAAAAAAGAGAACAACAAGGGACGGCGGAAGAAGAGA 1500 Db 1441 CCTTGAACTCGTGGCTGTAAGAAAAAGAGAACAACAAGAGGGCACGGCGGGAAGAAGA	Qy 1561 GAAGGAAGGCGATGTGTTCATCCCAGCAGCTCATCCAGTAGCCATCCTC 1620 Db 1561 GAAGGAAGGCGATGTTCATCATGCCAGCAGCTCATCAGTAGCCATCAACGCTTCCTC 1620 Qy 1621 CGAACTCCATCGGTTCGGTATCAACGCTGAAAAAAACAACCACAGAATCTTCCTTGC 1680 Db 1621 CGAACTCCATTGGTTTCGGTATCAACGCTGAAAAACAACCACAGAATCTTCCTTGC 1680	Qy 1681 AGGTGATAAGGACAATGTGATAGACCAGATAGAGAAGCAAGGAATTTAGCATTCCC 1740 Db 1681 AGGTGATAAGGACAATGTGATAGACCAGATAGAGAAGCAAGC	Oy 1801 TGCTCGTCCTCAATCTCAATCTCCGTCGTCTCTCTGAGAAGGTCTCCTGAGAA 1860	Qy 1921 TTTTAACTGAGATGGAGGCAACTTGTTATGTATCGATAATAAGATCACGCTTTTGTACT 1980 Db 1921 TTTTAACTGAGAATGGAGGCAACTTGTTATGTATCGATAATAAGATCACGCTTTTGTACT 1980 Qy 1981 CTACTATCCAAAAACTTATCAATAAAAAAAACGTTTGTGCGTTGTTTCTCC 2032 Db 1981 CTACTATCCAAAAACTTATCAATAAAAAAAACGTTTGTGCGTTGTTTCTCC 2032	RESULT 6 12-10-899-551-1 15 Sequence 1, Application US/10899551 16 Publication No. US20050063994A1 17 SERVERAL INFORMATION: 18 APPLICANT: Caplan, Michael J. 18 APPLICANT: Burks, A. Wesley 19 APPLICANT: Sampson, Hugh A.	APPLICANT: Howard, Soaln B. APPLICANT: Bottomly, Kim H. TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction to Allergy FILE REFERENCE: 2002834-0233 CURRENT APPLICATION NUMBER: US/10/899,551 CURRENT FILING DATE: 2004-07-26 NUMBER OF SEQ ID NOS: 61 SOFTWARE: PatentIn version 3.2	; SEQ 1D NO 1 ; SEQ 1D NO 1 ; LENGTH: 2032 ; TYPE: DNA ; ORGANISM: species Arachis hypogea US-10-899-551-1 Query Match Best Local Similarity 100.0%; Score 2032; DB 10; Length 2032; Best Local Similarity 100.0%; Pred. No. 0; Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ATANATCATATATATATATATATATATATATATATATATA

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iive 0; Mismatches
FILE REFERENCE: 072121/0104
CURRENT APPLICATION NUMBER: US/10/958,324
CURRENT FILING DATE: 2004-10-06
FRIOR APPLICATION NUMBER: US/09/715,036
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENT NOS: 8
LENGTH:: 2032
                                                                                                                                                                         TYPE: DNA
ORGANISM: Arachis hypogaea
US-10-958-324-5
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Best Local Similarity 100.
Matches 2032; Conservative
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Publication No. US20050114924A1
GENERAL INFORMATION:
APPLICANT: DODO, HORTENSE W.
APPLICANT: KONAN, KOFFI N'DA
APPLICANT: VIQUEZ, OLGA
APPLICANT: VIGUEZ, OLGA
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES ITILE OF INVENTION: TRANSGENIC PEANUT SEEDS
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Qy 1921 TTTTAACTGAGAATGGAGCAACTTGTTATGTATCGATAATAAGATCACGCTTTTGTACT 1980 Db 1921 TTTTAACTGAGAATGGAGCCAACTTGTTATCGATAATAAGATCACGCTTTTTGTACT 1980 Qy 1981 CTACTATCCAAAACTTATCAATAAAAAAAAATGTTGTGCGTTGTTTCTCC 2032 Db 1981 CTACTATCCAAAACTTATCAATAAAAAAAAAAAAAAAA	RESULT 8 US-10-100-303A-6 Sequence 6, Application US/10100303A Sequence 6, Application US/10100303A Sequence 6, Application US/10100303A Sequence 6, Application US/10030202980A1 GENERAL INFORMATION: TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction TITLE OF INVENTION: to Allergy FILE REFERENCE: 2002834-016 CURRENT APPLICATION NUMBER: US/10/100,303A CURRENT FILING DATE: 2002-03-18 SOFTWARE: PatentIN Ver. 2.1 SEQ ID NO 6 LENGTH: 1949 TYPE: DNA CREATION AT ARCHIS Hypogaea, Prot/Nucleo-Ara h 1	Ouery Match Query Match Best Local Similarity 95.0%; Pred. No. 0; Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 48 CAATGAGAGGAGGTTTCTCCACTGATGCTGTGGGATCCTTGTCTGGCTTCAG 19	0y 228 CTCGCTGCACCAAGCTCCAGTATGATCCTTGTTGTCTATGATCCTCGAGGACACATG 1
781 CGTGACCGTAGCAAATGGCAATAACAGAAGGCTTTAATCTTGACGAGGGCCATGCACT 840 841 CAGAATCCCATCGGTTTCATTTCCTACATCTTGAACGCCATGACAGAACCTCAG 900	961 GAGCAGCCGAGACCAATCATCTACTTGCAGGGCTTCAGCAGGAATACGTTGGAGGCCGC 1020	1201 AAAGAAAGGCTCCGAAGAGGGATTTTTTTTTTTTTTTTT	GGACGAAGACGAAGAGAGGAAGTAACAGAGGGGGGGGGG

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CACTCCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTGTTATGTATCGAT
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APPLICANT: Rapp, William
APPLICANT: Peng, Jiexin
APPLICANT: Nadig, Gautham
APPLICANT: Venkatesh, T
TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR
TITLE OF LING DATE: 2002-09-17
CURRENT APPLICATION UNMBER: US/10/245,227B
CURRENT PILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin version 3.1
SEQ ID NO 1254
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Pred. No. 4.2e-115;
0; Mismatches 382;
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Best Local Similarity 62.1%;
Matches 779; Conservative
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Sequence 13. Application US/10245227B
Publication No. US20030200558A1
GENERAL INFORMATION:
APPLICANT: Rapp, William
APPLICANT: Peng, Jiexin
APPLICANT: Nedig, Gautham
APPLICANT: Venkatesh, T
TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR THEIR USE

RESULT 10 US-10-245-227B-13

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Pred. No. 4.3e-115;
0; Mismatches 382;
FILE REFERENCE: REN-00-087-US
CURRENT APPLICATION NUMBER: US/10/245,2278
CURRENT FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 1278
TYPE: DNA
CORGANISM: Artificial sequence
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                                                         Score 406.8; DB 3;
Pred. No. 4.3e-115;
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  AAAGGCCATGGTTATCGTCGTCGTCAACAAAGGAACTGGAAACCTTGAACTCGTGGCTGT
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CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                        891 TAAAGAACAACAACAGAAGCAGAACAGGAAGAGGAACCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROFSOFT WORD 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTERBURY
REGISTRATION NUMBER: 30,971
REPERENCE/DOCKET NUMBER: BB-1071-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
CLASSIFICATION: CURKNOWN>
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LENGTH: 1320 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09758652 Patent No. US20010011377A1 GENERAL INFORMATION:
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TELEFAX: 302-773-0164
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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510 GTCCTACTTGCAAGGCTTCAGCCATAATATTCTAGAGACCTCCTTCCATAGCGAATTCGA
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                                                       TGAGATACGGAGGGTGCTGTTAGAAGAGAATGCAGGAGGTGAGCAAGAGGAGAGAGGCA
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ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAMARE
COUNTRY: UNITED STATES OF AMERICA
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APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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 ------GAAGTGCAAAGGTACAGAGCTGAATTGTCTGAAGACGATGTATT 1019
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Publication No. US20030200558A1
GENERAL INFORMATION:
APPLICANT: Rapp, Jiexin
APPLICANT: Peng, Jiexin
APPLICANT: Nengi, Gautham
APPLICANT: Nengi, Gautham
APPLICANT: Nengi, Gautham
APPLICANT: Nenkatesh, T
TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR THEIR USE
FILE REFERENCE: REN-00-087-US
CURRENT APPLICATION NUMBER: US/10/245,227B
CURRENT FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 83
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Pred. No. 4.3e-115;
0; Mismatches 382;
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62.1%;
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Best Local Similarity 62.1
Matches 779; Conservative
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; ORGANISM: Glycine max
US-10-245-227B-3
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US-10-245-227B-3
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                                                                                                                                   .219 AGAGGGAGATATCACCAACCCAATCAACTTGAGAAGGCGAGCCGAGCCGATCTTTCTAACAA
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CITY: WILMINGTON
STATE: DELAMARE
COUNTY: WILMINGTON
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TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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ZIP: 19898
COMPUTER READABLE FORM:
MEDLUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROFSOFT WORD 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WINDOWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ANTHONY JOHN KINNEY
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CORRESPONDENCE ADDRESS
ADDRESSEE: E. I. 1
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-684-651-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local S
Matches 779
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CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAAACCCACAGCTTCGGGACTTGGA
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TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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REDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/757,155
FILING DATE: 14-Jan-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UNITED STATES OF AMERICA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE
STREET: 1007 MARKET STREET
CITY: WILMINOTON
STATE: DELAWARE
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US-10-757-155-3
; Sequence 3, Application US/10757155
; Publication No. US20040139503A1
; GENERAL INFORMATION:
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Pred. No. 4.3e-115;
0; Mismatches 382;
                                                                                  FILING DATE: 11-Jan-2001

FILING DATE: 11-Jan-2001

APPLICATION NUMBER: 60/019,940

FILING DATE: JUNE 14,1996

ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY

REGISTATION NUMBER: 30,971

REFERENCE/DOCKET NUMBER: BB-1071-A

TELECOMMUNICATION INFORMATION:
TELEFAX: 302-92-92-481

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs

TYPEN INCLES SIGIL

STRANDEDNESS: single
                                                                        APPLICATION NUMBER: US/09/758,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%;
62.1%;
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Best Local Similarity 62.1
Matches 779; Conservative
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                                                                                                                                                                                                                                                      Score 406.8; DB 8;
Pred. No. 4.3e-115;
0; Mismatches 382;
        REGISTRATION NUMBER: 30, 971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPRONE: 302-773-0164
TELEPRA: 302-773-0164
FORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: CDNA; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-757-155-3
   NAME: LYNNE M. CHRISTENBURY
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62.1%;
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Best Local Similarity 62.1
Matches 779; Conservative
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  GATAGACCAGATAGAGAAGCAAGCGATTTTAGCATTCCCTGGGTCGGGTGAACAAGT
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Search completed: June 24, 2006, 01:56:13 Job time : 2781.65 secs

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Sequence 1, Appli
Sequence 34378, A
Sequence 5550, Ap
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Sequence 77435, A
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3. /EMC_Celerra_SIDS3/ptodata/l/pubpna/USO8_NEW_PUB.seq:*

4. /EMC_Celerra_SIDS3/ptodata/l/pubpna/PCT_NEW_PUB.seq:*

5. /EMC_Celerra_SIDS3/ptodata/l/pubpna/PCT_NEW_PUB.seq:*

5. /EMC_Celerra_SIDS3/ptodata/l/pubpna/USI0_NEW_PUB.seq:*

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                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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GenCore version (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                     nucleic search, using sw model
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                  US-10-449-902-25812
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US-10-449-902-1016
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US-10-449-902-23378
US-11-217-529-617
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DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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Pred. No. 2.2e-07;
D; Mismatches 204;
; Sequence 26870, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION: CENERAL INFORMATION: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA 1 TITLE OF INVENTION: ENCONDED THERBY FILE REFRENCE: 2750-1579PUS2; CURRENT APPLICATION NUMBER: US/10/953,349; CURRENT FILING DATE: 2004-09-30; NUMBER OF SEQ ID NOS: 40252; SOFTWARE: PatentIn version 3.3; SSQ ID NO 26870
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PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-38370
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 20667
LENGTH: 1295
                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AKO70973
DATABASE BUTRY DATE: 2001-12-06
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     2003-05-29
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SEQ ID NO 1
LENGTH: 1420
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Best Local Similarity 50.59
Matches 101; Conservative
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LOCATION: (1212)..(1212)
OTHER INFORMATION: n = a
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LOCATION: (77)..(1231)
     CURRENT FILING DATE:
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US-10-534-744-1
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US-10-534-744-1
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-AC205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR PRIOR DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-2383870
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7999
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Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Blo-oriented Technology Research Advancement in APPLICANT: The Institute of Physical and Chemical Research
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196 GICCCGGCAAGTICCAGTATITCT 820
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; Publication No. US20060123505A1
; GENERAL INFORMATION:
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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK105347
; DATABASE ENTRY DATE: 2002-08-28
] US-10-449-902-7999
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Best Local Similarity 46.0
Matches 157; Conservative
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US-10-449-902-20667
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Publication No. US20060122375A1

GENERAL INFORMATION:
APPLICANT: University of Saskatchewan Technologies Inc.
TITLE OF INVENTION:
FILE REFERENCE: 47968-PT

CURRENT APPLICATION NUMBER: US/10/534,744

CURRENT FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: US 60/426,012

PRIOR APPLICATE: 2002-10-14

NUMBER OF SEQ ID NOS: 4
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Query Match 2.1%; Score 43.4; DB 6; Length 1295; Best Local Similarity 53.9%; Pred. No. 0.0071; Matches 89; Conservative 0; Mismatches 76; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                        493 GCCCGAAGGAAGAAGAAGAACAAGAGTGGGGAACACCAGGTAG 537
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE OF INVENTION: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 38190
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                                                                                                                                                                                                                                                                                                                                                      675 TCCAGAATCACCGTATTGTGCAGATCGAGGCCAAACCTAACACTCTTGTTCTTCCCAAGC
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                                                                                                                                                                                                                                                                  Length 931;
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                                                                                                                                                                                                                                                                Score 41.6; DB 6;
Pred. No. 0.02;
0; Mismatches 129;
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Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                          TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK063700
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                  2.0%;
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 6550
                                                                                                                                                                                                                                                           2.0%
Best Local Similarity 48.0%
Matches 119; Conservative
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Matches 166; Conserv
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                                                                                       LENGTH:
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Publication No. US20060107345A1
GENERAL INFORMATION:
TOTALE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
                                           CTCCAGGGGAGCGGACACGTGGCCGCCAACCCGGAGACTACGATGATGACGCCGCCGTCAAC 368
  344 CTCCACATGGGGGGCGACCACAAAAATAAGGAGGAGGAGCACCACAAAAAAAGGCCGAGGAG 403
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Sequence 6550, Application US/10449902
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REPRENCE: MOA-A02051-108
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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Pred. No. 0.013;
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
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; LOCATION: (281)...(281)
; OTHER INFORMATION: n is a, c, g, or
US-10-953-349-34378
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LOCATION: (234)..(234)
OTHER INFORMATION: n is a,
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Matches 111; Conservative
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US-10-449-902-6550
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LENGTH: 726
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APPLICANT: Pagano, MICRELE
APPLICANT: Chiaur, Dah Sharim
APPLICANT: Latres, Esther
APPLICANT: Latres, Esther
APPLICANT: Latres, Esther
APPLICANT: Chaidwarker, Rajiv
TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-106-999
CURRENT APPLICATION NUMBER: 10/632,150
PRIOR APPLICATION NUMBER: 10/632,150
PRIOR APPLICATION NUMBER: 10/732,150
PRIOR FILING DATE: 2002-01-07
PRIOR FILING DATE: 1999-08-07
PRIOR FILING DATE: 1999-08-07
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR APPLICATION NUMBER: 60/124,449
PRIOR APPLICATION NUMBER: 60/124,449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 615;
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53.1%; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: modified base
LOCATION: (152)..(192)
OTHER INFORMATION: a, c, g, t, unknown, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                      CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 77435
LENGTH: 615
                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 93, Application US/11106014 Publication No. US20060088846A1 GENERAL INFORMATION:
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Matches 86; Conservative
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 93
LENGTH: 3489
     FILE REFERENCE: S-38-285
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436 GCGCCGTCGTCTGCCAACCACCAACACCAGTCGGAATGGTTCCGCGTCGTCATGCTCC 495
                                                                                                                 496 TCAGCCCCGTCGTCTCCACGTCTGGAGGACTTCTTCCCCATCGAGAGGAGGAG 555
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                                                                                     915 CCATGCC---CGTTAACACACCGGCCAGTTTGAGGATTTCTTCCCGGCGAGCAGCCGAG 971
                                                                                                                                                                                                                                                                                                                                                                              Sequence 9830, Application US/10449902
PUDIcation No. 1020060123505A1
GENERAL INFORMATION
PAPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FOLLI-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A02051-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR PELICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-06-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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                                                                                                                                                                                              972 ACCAATCATCCTACTTGCAGGCTTCAGCAGGAATACGTTGGAGGCCGCCTTCAA 1026
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APPLICANT: NAKAO, YOSHIHISO
APPLICANT: NAKAO, YOSHIHISA
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIWINEA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHKO
ITILE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107178
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa
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US-11-217-529-77435/c
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US-10-449-902-9830
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APPLICANT: AZINZAI, Yalda; BARROSO, Ines;
APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BOKOWSKY, Mark L.; DUGGAM, Brendan M.;
APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brendan M.;
APPLICANT: ELLIOTT, Vicki S.; EMERLING, Rimberly J.;
APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;
APPLICANT: GRIFFIN, Jennifer A.; ISON, Craig H.;
APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
APPLICANT: KABLE, Amy E.; KHAN, Farrah A.;
APPLICANT: KABLE, Amy E.; KHAN, Farrah A.;
APPLICANT: KABLE, Any E.; KHAN, Farrah A.;
APPLICANT: KABLE, Any E.; KHAN, Farrah A.;
APPLICANT: MARREN, Bridget A.; YU, Yuming;
APPLICANT: WARREN, Bridget A.; YU, Yuming;
APPLICANT: VUE, Huibin G.; YUE, Henry;
APPLICANT: YUE, Huibin BROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
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                                                                                                   1505 GAAGACGAAGAAGAGGAGGAAGTAACAGAGGTGCGTAGGTACACACCGGGGTTGAAG 1564
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                                                                                                                                                                                                                                     1565 GAAGGCGATGTTTCATCATGCCAGCAG 1592
                                                                                                                                                                                                                                                                                                1371 GAACTGGAAGGGATCCTGCTTCCGTCAG 1398
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CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/52/25465
PRIOR FILING DATE: 2002-08-02
PRIOR FILING DATE: 2002-08-03
PRIOR APPLICATION NUMBER: US 60/311,017
PRIOR APPLICATION NUMBER: US 60/313,070
PRIOR APPLICATION NUMBER: US 60/313,070
PRIOR PILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-31
PRIOR PRILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/316,692
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR PRILING DATE: 2001-08-31
PRIOR PRILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR PRIOR DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-07
PRIOR FILING DATE: 2001-12-07
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; OTHER INFORMATION: Incyte ID No: 7500176CB1
US-10-486-020-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/10486020 Publication No. US20060127894A1 GENERAL INFORMATION:
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SOFTWARE: PERL Program
SEQ ID NO 48
LENGTH: 2824
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                                                                 1476 AGAGGGGACGGCGGGAAGAAGAGGGGGGACGAAGACGAAGAGAGAGGGGAAGTAACAGAG 1535
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PRIOR APPLICATION NUMBER: DCT/US02/25465
PRIOR PILING DATE: 2004-02-05
PRIOR PILING DATE: 2004-08-02
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-17
PRIOR PLING DATE: 2001-08-24
PRIOR PLING DATE: 2001-08-24
PRIOR PLING DATE: 2001-08-31
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-14
PRIOR PLING DATE: 2001-09-14
PRIOR PLING DATE: 2001-10-07
PRIOR PLING DATE: 2001-10-05
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PRIOR PLING DATE: 2001-10-07
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
      0; Gaps
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1.9%; Score 39.2; DB 6; Length 1962;
Best Local Similarity 54.1%; Pred. No. 0.16;
Matches 80; Conservative 0; Mismatches 68; Indels 0
   0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: AZZMIZAL, Yalda; BARROSO, INES;
APPLICANT: AZZMIZAL, Yalda; BARROSO, INES;
APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BLIOTTY, Nark L.; DUGGAN, Brendan M.;
APPLICANT: ELIOTTY, Vicki S.; EMERLING, Brooke M.;
APPLICANT: GORVAD, Ann E.; GRAUL, Richard C.;
APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;
APPLICANT: HARALIA, April J.A.; ISON, Craig H.;
APPLICANT: KABLE, Amy E.; KHAN, Farrah A.;
APPLICANT: LEE, Sally; LEE, SOO Yeun;
APPLICANT: LIE, Sally; LEE, SOO Yeun;
APPLICANT: SWARNAKAR, Anita; TANG, Y. TOM;
APPLICANT: WARREN, Bridget A.; XU, Yuming;
APPLICANT: YOE, Whibin
APPLICANT: YUE, Whibin
                                                                                                                                                                                                                                                             2609 cagadegegerecaeccaecreaare 2638
                                                                                                                                                                                                1536 AGGTGCGTAGGTACACAGCGAGGTTGAAGG 1565
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, OTHER INFORMATION: Incyte ID No: 90081189CB1
US-10-486-020-52
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 52, Application US/10486020; Publication No. US20060127894A1; GENERAL INFORMATION:
   59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PERL Program
SEQ ID NO 52
LENGTH: 1962
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APPLICATION, AND DEATH
FILE REFERENCE: PF-1126 USN
CURRENT APLICATION NUMBER: US/10/486,020
CURRENT APPLICATION NUMBER: US/10/486,020
CURRENT FILING DATE: 2004-02-05
PRIOR PILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-17
PRIOR PELICATION NUMBER: US 60/311,017
PRIOR PELICATION NUMBER: US 60/313,070
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR PELING DATE: 2001-08-17
PRIOR PELING DATE: 2001-08-31
PRIOR PELING DATE: 2001-08-31
PRIOR PELING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-12-07
                                 1445 GAACTCGTGGCTGTAAGAAAAAGAGCAACAACAGGGGACGGCGGGAAGAAGAGAGAGGAC 1504
                                                                                                1494 GAGGATGAGGATGAGGATGAAGATGAGGATGAACGGCAGTTACTGGGAGAATTTGAGAAG 1553
                                                                                                                                                                               1505 GAAGACGAAGAAGAGGAGGAAGTAACAGAGAGGTGCGTAGGTACACACAGCGAGGTTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: AZIMZA, Yalda; BARROSO, Ines;
APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BOROWSKY, Mark L.; DUGGAN, Brendan M.;
APPLICANT: ELILOTT, Vicki S.; EMERLING, Brooke M.;
APPLICANT: GORYAB, Ann E.; GRAUM, Richard C.;
APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;
APPLICANT: HAPALIA, April J.A.; ISON, Craig H.;
APPLICANT: LEE, Sally; LEE, Soo Yeun;
APPLICANT: LEE, Sally; LEE, Soo Yeun;
APPLICANT: RICHARDON, Thomas W.; SPRAGUE, William W.;
APPLICANT: RICHARDON, Thomas W.; SPRAGUE, William W.;
APPLICANT: WARREN, Bridget A.; XU, Yuming;
APPLICANT: YAO, Mondque G.; YUE, Henry;
                                                                                                                                                                                                                                                                                                                         1565 GAAGGCGATGTGTTCATCATGCCAGCAG 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7510095CB1
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OTHER INFORMATION: Incyte
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SEQ ID NO 53
LENGTH: 3005
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TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PF-1126 USN
CURRENT APPLICATION UNMBER: US/10/486,020
CURRENT FILING DATE: 2004-02-05
PRIOR PELICATION NUMBER: PCT/US02/25465
PRIOR PELING DATE: 2001-08-08
PRIOR PELING DATE: 2001-08-08
PRIOR PELING DATE: 2001-08-17
PRIOR PELING DATE: 2001-08-21
PRIOR PELING DATE: 2001-08-21
PRIOR PELING DATE: 2001-09-17
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                                         1447 GAGGATGAGGATGAGGATGAGGATGAGGATGAACGGCAGTTACTGGGAGAATTTGAGAAG 1506
1505 GAAGACGAAGAAGAGGAAGGAAGTAACAGAGGTGCGTAGGTACACAGCGAGGTTGAAG 1564
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SOFTWARE: PERL Program
SEQ ID NO 54
LENGTH: 2906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: AZIMZAL, Yalda, BARROSO, Ines;
APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BACGWSKY, Mark L.; DUGGAN, Brendan M.;
APPLICANT: BOROWSKY, Mark L.; DUGGAN, Brendan M.;
APPLICANT: FORSYTHE, Ian J.; GIETZEN, Kimberly J.;
APPLICANT: GORVAD, Ann E.; GRAUL, Richard C.;
APPLICANT: GRIFFIN, Jennifer A.; GURURAJAN, Rajagopal;
APPLICANT: HAPALIA, APRIL J.A.; ISON, Craig H.;
APPLICANT: LEE, Sanly: LEE, Soo Yeun;
APPLICANT: RICHARDON, Thomas W.; SPRAGUE, William W.;
APPLICANT: SWARNAKAR, Anite; TANG, Y. Tom;
APPLICANT: YOU, Monique G.; YUE, Henry;
APPLICANT: YUE, Huibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7510096CB1
                                                                                                                                                                                                                                                                                    1565 GAAGGCGATGTTTCATCATGCCAGCAG 1592
                                                                                                                                                                                                                                                                                                                                                       1507 GAÁCTGGAAGGGATCCTGCTTCCGTCAG 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54, Application US/10486020
Publication No. US20060127894A1
GENERAL INFORMATION:
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Matches 80; Conservative
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US-10-486-020-54
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US-10-486-020-53

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                                           1445 GAACTCGTGGCTGTAAGAAAAGAGCAACAACAGGGGGACGGGGGAAGAAGAGGGGGC 1504
                                                                1505 GAAGACGAAGAAGAGGAGGGAAGTAACAGAGGTGCGTAGGTACACAGCGAGGTTGAAG 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 GCTGGACCGAGGGAGCGTGAAAGAGAAGAAGACTGGAGACAACCAAGAGAAGATTGGAGG 460
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Query Match
1.9%; Score 39.2; DB 6; Length 3005;
Best Local Similarity 54.1%; Pred. No. 0.21;
Matches 80; Conservative 0; Mismatches 68; Indels 0.
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5994
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AF066463 Sequence
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Burks, A. W. Jr., Stanley, J.S., Cockrell, G., King, N.E., Sampson, H.A., Helm, R.M. and Bannon, G.A.
Peanut allergens and methods
Patent: US 6486311-A 20 26-NOV-2002;
Wt. Sinai School of Medicine and University of Arkansas; New York, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAG 120
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Best Local Similarity 100.0%; Pred. No. 9e-202;
Matches 717; Conservative 0; Mismatches 0; Indels
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Sequence 20 from patent US 6486311.
AR257468.1 GI:27307481
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    717 / Organism="unknown"
/mol_type="genomic DNA"

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AY848699
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AR629100 Sequence
A77197 Arachis hyp
AR277462 Sequence
AY72689 Arachis h
AY581853 Arachis h
AY581854 Arachis h
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AX155333 Sequence
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AX107229 Arachis h
AR716327 Sequence
AX148740 Sequence
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                                                                                                                                              June 23, 2006, 09:32:31 ; Search time 4184.37 Seconds (without alignments) 10957.506 Million cell updates/sec
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                      GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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Burks, A.W. Jr., Stanley, J.S., Bannon, G.A., Cockrell, G. Helm, R.M.

Peanut allergens and methods

Patent: US 6835824-A 9 28-DEC-2004;

University of Arkansas; Little Rock, AR
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100.0%; Score 717; DB 2;
Best Local Similarity 100.0%; Pred. No. 9e-202;
Matches 717; Conservative 0; Mismatches 0;
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Sequence 9 from patent US 6835824.
AR629100 GI:59756577
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Unclassified.
1 (bases 1 to 717)
Burks,A.W. Jr., Stanley,J.S., Bannon,G.A., Cockrell,G. and Helm,R.W.
Helm,R.W.
Paneut allergens and methods
Patent: US 6835824-A 6 28-DEC-2004;
University of Arkansas; Little Rock, AR
Location/Qualifiers
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Sequence 6 from patent US 6835824
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1 (bases 1 to 743)
Burks,A.W. Jr., Stanley,J.S., Cockrell,G., King,N.E., Sampson,H.A.,
Helm,R.M. and Bannon,G.A.
Peanut allergens and methods
Patent: US 6486311-A 1 26-NOV-2002
Mt. Sinai School of Medic.
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Seguence 1 from patent US 6486311.
AR257462.1 GI:27307475
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Arachis hypogaea (clone Ara h II p38) a
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/mol_type="genomic DNA"
/strain="Florunner"
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/clone="Ara h II p38"
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y and Biotechnology, 510275, China

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/product="25 protein 1"
/protein id="AAU21494 1"
/db_xref="id="AAU21494 1"
/db_xref="d1:52001227"
/translation="GRGKHHTLFNTHSITTTTTMAKLTILVALALFLLAAHASARQQW
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SSQHQERCCNELNEFENNUGRCMCEALQQIMENQSDRLQGRQGEQGFKRELRNLPQQCG
LRAPQRCDLDVESGSRRRY"
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   clone of peanut seed storage protein gene
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llarity 99.9%; Pred. No. 3.4e-198;
Conservative 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:3818"
                                                                                                                                                                                                               protein"
               Unpublished
3 (bases 1 to 810)
Yan,Y., Wang,L. and Huang,S.
Direct Submission
Submitted (30-JUL-2004) Department
Sun Yat-sen University, GuangZhou,
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/note="seed storage
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Matches 716; Conserv
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
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1 (bases 1 to 810)

Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.:
Explation of peanut genes encoding arachins and conglutins plant Sci. 169 (2), 439-445 (2005)

2 (bases 1 to 810)
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     Length 743;
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Score 713.8; DB 2;
Pred. No. 8.1e-201;
0; Mismatches 2;
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Yan,Y., Wang,L. and Huang,S.
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Query Match
Best Local Similarity 99.7%;
Matches 715; Conservative
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Length 810; Indels 127 120 187 180 247 240 307

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/translation="DHTLFNTHS1TTTTTMAKLT1LVALALFLLAAHASARQQWEFQG
DRRCQSQLERANLRPCEQHLMQKIQRDEDSYERDPYSPSQDPYSPSPYDRRGAGSSQH
QERCCNELNEFENNQRCMCEALQQIMENQSDRLQGRQQEQOFKRELRNLPQQCGLRAP
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Arachis hypogaea seed storage protein SSP2 mRNA, partial cds.
AYS81854
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Direct Submission
Submitted (01-MAR-2004) Department of Biology and Biotechn School of Life Science, Sun Yat-sen University, GuangZhou, GuangDong 510275, China
Location/Qualifiers
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/protein_id="AAT00599.1"
/db_xref="G1:46560482"
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/cultivar="SanYou523"
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Arachis hypogaea seed storage protein SSP1 mRNA, partial cds.
AYS81853
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pydrrgagssohoerccnelnefennorcmcealooimenosdrlogroopekrel
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Direct Submission
Submitted (01-MAR-2004) Department of Biology and Biotechnology,
School of Life Science, Sun Yat-sen University, GuangZhou,
GuangDong 510275, China
Location/Qualifiers
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1 (bases 1 to 842)
Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.Z.
Isolation of peanut genes encoding arachins and conglutins by expressed sequence tags
Plant Sci. 169 (2), 439-445 (2005)
Z. (bases 1 to 842)
Yan, Y., Wang, L. and Huang, S.
CDNA clone of peanut seed storage protein gene
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37;
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/db_xref="G1:46560480"
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/db_xref="taxon:3818"
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Patent: WO 0140264-A 6 07-JUN-2001;
Panacea Pharmaceuticals, LLC (US) ; The University of Arkansas (US)
Panacea Pharmaceuticals, LLC (US) ; The University of NEW YORK (US)
                                                   C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/00,C12N15/00,C12N5/
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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HAWADO SOSIN,GARY A BANON,WESLEY A BIRX JR,HYU A SAMPTHON PC
5/09,A01H5/00,A01K67/027,A61K39/35,C07K14/37,C07K14/415, PC
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                                                                                  decreasing allergic reactions
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                                                                                    reagents for decreated Location/Qualifiers
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/organism="unidentified"
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Methods and reagents for decreasing allergic reactions.
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unclassified sequences.

S Sosin, H. Danon, C.A., Jr. W.A.B. and Sampthon, H.A.

S Sosin, H. Danon, C.A., Jr. W.A.B. and Sampthon, H.A.

S Sosin, H. Banon, C.A., Jr. W.A.B. and Sampthon, H.A.

Methods and reagents for decreasing allergic reactions

L Patent: JP 2002501748-A 2 22-JAN-2002;

UNIVERSITY OF ARRANSAS, MOUNT SINAI SCHOOL OF MEDICINE OF THE CITUMINESITY OF NEW YORK, HOWARD SOSIN

OS Arachis L. (Peanut)

PP 32-JAN-1999 JP 2000529437

PP 29-JAN-1999 US 60/073624,13-FEB-1998 US 60/074633 PR

13-FEB-1998 US 60/074624,13-FEB-1998 US 60/074633 PR
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                                                        Gaps
                                                      ..
7
                     Length 678;
                                                      Indels
                 Score 598.8; DB 4;
Pred. No. 1.4e-166;
0; Mismatches 2;
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                     Query Match
Best Local Similarity 99.4%;
Matches 622; Conservative
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DEFINITION
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BD107899
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1 (bases 1 to 472)
Viquez,O.M., Summer,C.G. and Dodo,H.W.
Isolation and molecular characterization of the first genomic clone
of a major peanut allergen, Ara h 2
J. Allergy Clin. Immunol. 107 (4), 713-717 (2001)
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Arachis hypogaea
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae,
Aeschynomeneae, Arachis.
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Direct Submission
Submitted (16-AUG-2000) Food and Animal Sciences, Alabama A&M
University, Meridian Street, 4900, Normal, AL 35762, USA
Location/Qualifiers
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                                                            'organism='Arachis hypogaea (peanut)'.
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0
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AY007229
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                                                                                                                                                                                                                        65.7%; Score 470.8; DB 2; 99.6%; Pred. No. 1.7e-128;
seed storage protein and allergen
Key Location/Qualifiers
                                                                                                  1. .474
/organism="Arachis hypogaea"
/mol_type="genomic DNA"
/db_xref="taxon:3818"
                                                                                                                                                                                                                                                                0; Mismatches
                                       1. .474
                                                                                 Location/Qualifiers
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Matches 472; Conserv
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Wharrycus, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids 1, Fabales, Fabaceae, Papilionoideae,
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Strandedness: Double;
Topology: Linear;
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1. (bases 1 to 474)
Jr.W.A.B., Helm,R.M., Cockrell,G., Steven, Stanley,J. and
Bannon,G.A.
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PN JP 200223783-A/1
PN JP 2002223783-A/1
PP 13-AUG-2002
PP 21-NOV-2001 JP 2001356754
PR 29-DEC-1995 US 60/009.455,04-MAR-1996 US 08/61
WESLEY A BURKS JR.RICKI M HELM,GAEL COCKRELL,STEVEN PI
STANLEY,GARY A BANNON
                                                                                                                                      Length 474;
                                                                                                                                                                              Indels
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                                                                                                                                      65.9%; Score 472.4; DB 2; 99.8%; Pred. No. 5.5e-129; ive 0; Mismatches 1;
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Patent: JP 2002223783-A 1 13-AUG-2002;
UNIVERSITY OF ARKANSAS

    .474
    forganism="Arachis hypogaea"
|mol_type="unassigned DNA"
|db_xref="taxon:3818"

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Location/Qualifiers
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BD172108
BD172108.1 GI:28413406
JP 200223783-A/1.
Arachis hypogaea (peanut)
                                                                                                                                                                                Conservative
                                                                                                                                                             Similarity
                                                                                                                                                                            473;
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BD172108
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PAT 08-JUN-2001
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Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                                                                                      121 GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA
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llarity 100.0%; Pred. No. 7.3e-126;
Conservative 0; Mismatches 0;
                             64.4%; Score 462; DB 2; Le
100.0%; Pred. No. 7.3e-126;
ive 0; Mismatches 0;
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Sequence 3 from Patent WO0136621.
AX148740 GI:14347294
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/db_xref="GI:1818705"
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RCMCEALQQIMENQSDRLQGRQQEQGFKRELENNLPQQCGLRAPQRCDLDVESGG"
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Dodo, H.W., Arntzen, C.J., Viquez, O.M. and Konan, K.N.
Down-regulation and silencing of allergen genes in transgenic
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          /organism="Arachis hypogaea"
/mol_type="genomic DNA"
/db_xref="taxon:3818"
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Patent: US 6943010-A 3 13-SEP-2005;
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Sequence 3 from patent US
AR716327
                                                                                                                  /note="Ara hII"
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                                                    CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG 240
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Dodo', H.W., Arntzen, C.J., Viquez, O.M. and Konan, K.N.
Dodo-i, H.W., Arntzen, C.J., Viquez, O.M. and Konan, K.N.
Down-regulation and silencing of allergen genes in transgenic peanut seeds
Patent: US 6943010-A 1 13-SEP-2005;
Location/Qualifiers
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100.0%; Pred. No. 7.9e-126;
iive 0; Mismatches 0;
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Sequence 1 from patent US 6943010.
AR716326 1 GI:77364701
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Best Local Similarity 100.
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GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG
                                                         GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAG
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Adg44001 G.max 2S Aat86281 Soybean a Aaz08720 Chimeric

Abd3339 Human can Ab12835 Nuclectid Ab15835 Nuclectid Ab168186 Human ost Aaf87134 Lunasin c Aaf87135 Lunasin c Ab132103 Human imm Ab13226 Human imm Ab13226 Human imm Ab184796 Human cDN Ad27131 Human imm Abk8333 DNA trans Abk28392 DNA trans Abc88133 Human ost Ad77147 Type II d Ad84181 Human lym Ad845353 Chemicall Abk28186 DNA trans Continuation (5 of Ab65284 Human can Ac160109 Human can Ac160109 Human can

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Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody; ELISA; analysis; Ara hII; ds.
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site monoclonal antibody based ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bannon GA
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AAF83654
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              AAT76615 standard; cDNA
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P-PSDB; AAW24153.
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polyA_signal
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04-MAR-1996;
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29-DEC-1997
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Aat76615 Peanut al
Aat76614 Peanut al
Adv97531 Peanut Ar
Adv97602 Peanut Ar
Aas06383 Peanut Ar
Aas06389 Peanut al
Aas08538 DNA encod
Abx70606 Peanut Ar
Adg27517 Peanut al
Aaf90337 Peanut al
Aaf90336 Peanut al
Aaf90336 Peanut al
Aat86282 Soybean a
Aat86282 Soybean a
Aat86283 Chimeric
Aax25346 Soybean a
Adh89268 G. max 28
Ad99268 G. max 28
                                                             (without alignments)
15647.278 Million cell updates/sec
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       GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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                                          which contains multiple IgE-binding epitopes. It was amplified from a peanut seed cDNA library using a primer (see AAT58683) based on an isolated Ara hil peptide (see AAW24151). The sequence shows significant homology with the conglutin family of seed storage proteins of other legumes. The gene is capable of producing a protein product in prokaryotic cells that is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hil and Ara hi see AAW24149-50) can be used to raise monoclonal antibodies which are used in a specific two- site MAD ELISA for the detection of Ara hi or Ara hil (laimed). IgE-binding Ara hil antigen epitopes (see AAW24188- 33) may be used in vaccines to protect against allergic reactions to peanut standardise OS field)
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                                   peanut allergen Ara hII (AAW22153),
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                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                   cDNA clone codes for the major
 Claim 31; Page 196; 354pp; English
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 717; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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This cDNA clone, designated p18, codes for the major peanut allergen Ara hII (AAW22164), which contains multiple 1gE-binding epitopes. It was amplified from a peanut seed cDNA library using a primer (see AAM28683) based on an isolated Ara HII peptide (see AAW24151). The sequence shows significant homology with the conglutin family of seed storage proteins of other legumes. The gene is capable of producing a protein product in prokaryotic cells that is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara HII and Ara HI (see AAW24195-50) can be used to raise monoclonal antibodies which are used in a specific two-site MAb ELISA for the detection of Ara HI or Ara HII (claimed). IgE-binding Ara HII antigen epitopes (see AAW24188-93) may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                  Peanut; seed storage protein; allergen; allergy; hypersensitivity; vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody;
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ilarity 100.0%; Pred. No. 7e-178;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 31; Page 183-185; 354pp; English.
                                                                                         Peanut allergen Ara hII cDNA clone P38.
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96US-00610424.
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This invention relates to a novel isolated nucleic acid molecule encoding the peanut allergen Ara h I that has been identified in patients with a topic dermatitis. Specifically, it refers to a monoclonal antibody expecifically, it refers to a monoclonal antibody enzyme-linked immunosorbant assay (ELISA) used to detect and quantify the peanut allergen antipen. The present invention also describes by ridomas that produce two-site monoclonal antibodies specific for a peanut allergen that can be used in an ELISA to detect and determine the concentration of a specific peanut allergen in a food product or in food processing. Furthermore, it provides an expression vector and the isolated nucleic acid or its fraction can include a diagnostic label. Accordingly, these nucleic acids are useful for obtaining diagnostics with optimal concentrations of each allergen or for developing panels of mixtures of large numbers of recombinant allergens such that it can be used in immunotherapy for the treatment of food hypersensitivity reactions. This polynucleotide sequence is the peanut Ara h II allergen CONA (PSB clone) of the invention. NB. This sequence is identical to that
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                                                                                                                                                                                                                                                                                                                                                                      ADV97541 standard; cDNA; 717
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-045982/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arachis hypogaea
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mixtures of large numbers of recombinant allergens such that it can be used in immunotherapy for the treatment of food hypersensitivity reactions. This polynucleotide sequence is the peanut Ara h II allergen cDNA (P38 clone) of the invention. NB. This sequence is identical to that identified as SeqID 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540
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immediate type hypersensitivity; Ara h II; dermatological; antiallergic;
                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITGITGCTGCAGAGTIGTAACCATCTIGAAATAATATAAAAAAAAGAICATGTTTTGTT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rrigingcigcagagingnaaccarcingaaaraararaaaagarcargiriffer 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ATCCTCTCACCACCAAGAGGGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAG
                                                                                                                                                                                                                                                                                                 1 ścicaccaracrastascecercsecerrirecrecrecrececaesearersesas
                                                                                                                                                                                                                                                                                                                                          GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGGGAACCTGAG
                                                                                                                                                                                                                                                                                                                                                                           61 GCAGTGGGAACTCCAAGGAGAACAAGAAGATGCCAGAGCCAGCTCGAGAGGGGCGAACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCCTCTCAGCACCAAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCCGGCAGAGACAGATACTAAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTATGTTTAGTTTTGGTAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTAAGGCAAGCTTAGGTTATATGAGCACCTTTAGAGTGCTTTTATGGCGTTGTCTATGT
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                , 0
                                                                                                                                                                         Length 717;
                                                                                                                                Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peanut Ara h II allergen clone P38 cDNA encoding a seed
                                                                                                                                                                     ; Score 717; DB 14;
; Pred. No. 7e-178;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                         100.0%;
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                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 717; Conservative
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360 365 420 425

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hypogea. The Ara h 2 protein has 10 IgE (Immunoglobulin E) binding epitopes, three of which are immunodominant (AAY15272, AAY15275, and AAY15275). By modifying the IgE binding sites the ability of the allergen to provoke an immune response is downregulated. The epitopes of the IgE binding sites can therefore be modified in genetically engineered plants and animals to elicit less of an allergic response. (Updated on 17-OCT-2003 to standardise OS field)
                                             246 ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAG
                                                                                                    GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG
                                                                                                                                         GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG
                                                                                                                                                                                 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAG
                                                                                                                                                                                                                           GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAAGTGCGGCCTTAG
                                                                                                                                                                                                                                                                                   This is the nucleotide sequence of the Ara h 2 protein from Arachis
                                                                                                                                                                                                                                                                GGCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCAGAGACAGATACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified allergen with reduced IgE binding, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 474; DB 2; Le 100.0%; Pred. No. 3.8e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lmmunoglobulin E; Ig E; binding site; peanut; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic; allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYAR-) UNIV ARKANSAS.
(UYNY ) UNIV NEW YORK MT SINAI SCHOOL MEDICINE.
(SOSI/) SOSIN H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sampson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 37; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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98US-0074590P.
98US-0074624P.
98US-0074633P.
98US-00141220.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peanut allergen, Ara h 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sosin H, Bannon GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-479189/40
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Best Local Similarity
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13-FEB-1998;
13-FEB-1998;
13-FEB-1998;
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09-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergy;
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(SOSI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel isolated nucleic acid molecule encoding the peanut allergen Ara h I that has been identified in patients with a topic dermatitis. Specifically, it refers to a monoclonal antibody enzyme-linked immunosorbant assay (ELISA) used to detect and quantify the enzyme-linked immunosorbant assay (ELISA) used to detect and quantify the peanut allergens, where the monoclonal antibodies have specificity for a selected peanut allergen antigen. The present invention also describes hybridomas that produce two-site monoclonal antibodies specific for a peanut allergen in a food product or in food processing. Furthermore, it provides an expression vector and the processing. Furthermore, it provides an expression vector and the solated nucleic acids are useful for obtaining diagnostic set with optimal concentrations of each allergen or for developing panels of mixtures of large numbers of recombinant allergens such that it can be used in immunotherapy for the treatment of food hypersensitivity reactions. This polynucleotide sequence is the peanut Ara h II allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGG 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid encoding peanut allergen Ara h 1, useful for obtaining diagnostics with optimal concentrations of each allergen, for developing panels of mixtures of recombinant allergens, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCCACGCATCTGCGAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCCACGCATCTGCGAGGCA
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immunosuppressive; antibody engineering; ss; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%; Score 475; DB 14; I
100.0%; Pred. No. 2.1e-114;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ö
                                                                                                                                     /partial
/product= "Ara h II protein"
/note= "Start codon is absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cockrell
                                                                             cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 27; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bannon GA,
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96US-00717933.
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Best Local Similarity 100.
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/*tag=
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                                     Arachis hypogaea.
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26-MAR-2003 (first entry)
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(UYAR-) UNIV ARKANSAS.
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27-SEP-2000;
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The sequence represents the coding sequence of anaphylactic antigen Ara h 2 is an anaphylactic antigen (A), which was used to design antigenic peptides having a reduced ability to bind immunoglobulin E (19E) as compared with the intact (A), or having a sequence substantially identical to a portion of sequence of an antigen that includes at least one 1gE binding site of the peptide is altered. The antiqenic peptides are used in a composition which is useful for reducing risk or severity of allergic reaction to an antigen. This is done by identifying an individual at risk of allergic reaction to an antigen by identifying prior display of allergic symptoms when exposed to the antigen. The antigen-specific 1gE present on one or more mast cells or basophils in the individual's serum is identified. The individual is then contacted with a peptide corresponding to a portion of the antigen. Which is selected, formulated, and delivered so that binding of the peptide to antigen-specific 1gE ireduced as compared with 1gE binding confined that the individual is reduced as compared with 1gE binding of intact antigen. The composition is also useful for treating and
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Antigenic fragments useful for reducing anaphylactic risk and reducing the severity and/or number of allergic symptoms in individuals sensitive to antigens, have reduced ability to bind Immunoglobulin E.
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                                                                                                                                             English
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                                                                                                                                             Disclosure; Fig 10;
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CAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAGG 420
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                                                                                                                                                                                                                                          474
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                                                                                                                                                                                                         GCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCAGAGACAGATACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peanut; plant; ss; gene; allergen; Ara h1; Ara h2; Ara h3; glycinin A2Bla; Jug n1; antiallergic; vulnerary; anaphylactic food allergen; IgE; allergy; wound.
                                                                                                                                                                                                                                                                                                                                     ADG27517 standard; cDNA; 474 BP
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96US-00717933.
98US-0074528P.
98US-0074624P.
98US-0074631P.
98US-00141220.
98US-00191593.
99US-0024057.
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CONNAUGHTON C.
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KING N E.
KOPPER R A.
MALEKI S J.
RABJOHN P A.
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SAMPSON H.
BANNON G A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KOPP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BANN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BURK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KING/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAMP/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a modified anaphylactic food allergen has an amino acid sequence that is substantially identical to that of natural anaphylactic food allergen, except for a cysteine residue that has been modified so that it cannot participate in the disulphide bond. The modification may also comprise mutation of the IgE binding sites to reduce allergenicity. Also included are: (1) a method of making a modificat anaphylactic food allergen; (2) a nucleotide molecule encoding or for causing a site specific mutation in the modified anaphylactic food allergen; (2) a nucleotide molecule encoding or for causing a site specific mutation in the modified anaphylactic food allergen; (4) a method of treating an individual by reducing the clinical response to a natural anaphylactic food allergen; anaphylactic food allergen is useful for preventing or treating allergen; cand an isolated fragment of peanut allergen such as food, insect, reactions associated with any natural allergens such as food, insect, treating wounds in mammals such as bovine, cannot, feline, caprine, ovine, porcine, mutine or equine species. The present sequence is a CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGGGAACCTGAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                     Caplan M, Sosin H, Sampson H, Bannon GA, Burks WA, Cockrell G;
Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;
Rabjohn PA, Shin DS, Stanley JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New modified anaphylactic food allergen, useful for preventing or
treating allergic reactions associated with e.g. anaphylactic allergens.
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                                                    Peanut, ss; allergy, Ara h1; Ara h2, Ara h3; gene; IgE binding site, anaphylactic food allergen; antiallergenic; vaccine; wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.1%; Score 474; DB 8; Length 474; Best Local Similarity 100.0%; Pred. No. 3.8e-114; Matches 474; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding a peanut allergen (e.g. Ara hl, h2 or h3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Fig 40; 300pp; English.
                                                                                                                                                                                                                                                            16-MAR-2001; 2001US-0276822P.
18-MAR-2002; 2002US-00276822.
                                                                                                                                                                                                                         18-MAR-2002; 2002WO-US009108
                                                                                                                                                                                                                                                                                                                    (PANA-) PANACEA PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-018765/01.
P-PSDB; ABU52464.
                   Peanut Ara h2 cDNA.
                                                                                                        Arachis hypogaea.
                                                                                                                                               WO200274250-A2.
                                                                                                                                                                                    26-SEP-2002
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WO200136621-A2
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                                                                                                                                                                                                                                           11-SEP-2003
23-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dodo HW,
                                                                                                                                                                        à
                                                                                                                                                                                                                                                                        The invention relates to a modified anaphylactic food allergen whose anaphylactic food allergen. The natural anaphylactic food allergen in cluddes at least one cysteine residue that participates in a disulphide bond when the natural anaphylactic food allergen is in its native conformation, except that the cysteine residue has been modified so that it cannot participate in the disulphide bond. Also included are a method of making a modified anaphylactic food allergen, a nucleotide molecule for causing a site specific mutation in a gene encoding a natural anaphylactic food allergen, a transgenic plant or animal expressing a modified anaphylactic food allergen defined above, a nucleotide molecule for causing a site specific mutation in a gene encoding a natural anaphylactic food allergen defined above, a natural anaphylactic food allergen by reducing the clinical response to a natural anaphylactic food allergen by administering a modified anaphylactic food allergen and isolated fragment of peanut allergen and an isolated fragment of peanut allergen series of the amino acids have been modified in at least one IgE epitope or all the IgE epitopes recognised when the natural anaphylactic food allergen and an isolated with serum IgE from individual (s) allergen pugn Jugn in. The modified anaphylactic food allergen and an individual consecutive anaphylactic food allergen and an individual consecutive and their encoding consecutive anaphylactic food allergen and an additied anaphylactic food allergen and an add
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                 Sampson H, Bannon GA, Burks AW, Cockrell G;
ton C, Helm RM, King NE, Kopper RA, Maleki SJ;
Stanley JS;
                                                                                                                                                                     New modified anaphylactic food allergen comprising a cysteine residue which has been modified so that it cannot participate in the disulfide bond, useful for treating allergic reactions or wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCACCATACTAGTAGCCCTCGCCCTTTTCCTCGCTGCCCACGCATCTGCGAGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treating allergic reactions or wounds. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 474; DB 10; Length 474;
Pred. No. 3.8e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. J. J. Matches 474; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encodes a Peanut allergen of the invention.
                                                                                                                                                                                                                                              Example 10; SEQ ID NO 62; 194pp; English.
                                                                   Compadre CM, Connaughton
Rabjohn PA, Shin DS, Sta
                                                   Sosin HB
(SHIN/) SHIN D S.
(STAN/) STANLEY J S.
                                                                                                                         WPI; 2003-875632/81
                                                                                                                                           P-PSDB; ADG27518
                                                   Caplan MJ, S
Compadre CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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The present sequence is that of the peanut allergen Ara h2 gene coding region. A portion of the Ara h2 gene is homologous to corresponding regions of the peanut allergen Ara h6 and Ara h7 genes. This region has comen for a manifered by the and Ara h7 genes. This region has considered by the and antisense orientations and used to down-regulate Ara h2, Ara considered and antisense orientations and used to down-regulate Ara h2, Ara condition, which relates to the production of a peanut plant having reduced, or undetectable, allergenic protein (AP) content in its seed. A contines and/or sense AP gene, or their fragments, regenerated antisense AP gene and/or sense AP gene, or their fragments, regenerated antisense AP gene, or their fragments, regenerated to plants, and fertile transgenic plants that produce seeds with reduced AP content are identified. The AP sense or antisense gene may comprise at the approach of the Ara h2 gene. The seeds are useful for preparation class are the foods. (Updated on 11-SEP-2003 to standardise OS field)
                                         420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peanut; allergen; Ara h2; Ara h6; Ara h7; transgenic plant; allergy; ds.
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361 CAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAGG
                                                                                                                                             422 GCACCACAGGGTTGCGACTTGGACGTCGAAAGTGGCGGCAGAGACAGATACTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "PCR amplified fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peanut allergen Ara h2 gene.
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/*tag= a
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b
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321. .528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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Konan KN, Viquez OM;

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Arntzen CJ,
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     Dodo HW,
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                                                              GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGACCAGCTCGAGAGGGCGAACCTGAG 120
                                                                                                                                                                                                    GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG 360
                                                                                                                                                                                                                                               GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAG 486
                                                                                                                                                                                  ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAG 366
                                                                        GCAGTGGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGCGAACCTGAG
                                                                                                GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA
                                                                                                         GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA
                                                                                                                                 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG
                                                                                                                                                ATCCTCTCAGCACCAAGAGGGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAG
                                                                                                                                                                                                                                     GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAG
                             GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCCACGCATCTGCGAGGCA
              Gaps
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            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Peanut; allergen; Ara h2; transgenic plant; allergy; ds.
                                                                                                                                                                                                                                                                       GGCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCAG 462
                                                                                                                                                                                                                                                                               GGCACCACCAGGGTTGGGACTTGGACGTCGAAAGTGGCGGCAG 528
     Pred. No. 6.3e-111;
100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 AAF90336 standard; DNA; 1162
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110. .172
/*tag= c
172. .730
/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                                           Peanut allergen Ara h2 gene.
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110. .733
             Matches 462; Conservative
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                  (revised)
    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             Arachis hypogaea
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23-JUL-2001
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The present sequence is that of the peanut allergen Ara h2 gene. The gene was identified following screening of genomic DNA using a probe (see AAB9042) based on the known Ara h2 coDNA sequence, subcloning of positive clones into a phagemid vector, restriction enzyme digestion, ligation with vector DNA, Southern hybridisation and sequencing. The gene encodes 20.7-amino acid allergenic protein (see AAB9283). The invention relates to a method for producing a peanut plant having reduced, or undetectable, allergenic protein (AP) content in its seed. A peanut plant cell is transformed with a DNA construct containing an antisense AP gene and/or sense AP gene, or their fragments, respensed to plants, and fertile transgenic plants that produce seeds with reduced AP content are identified. The AP sense or antisense gene may comprise at least a portion of the present sequence. The seeds are useful for preparation of allergen-free foods. Recombinant AP may be produced and used to produce antibodies useful for detecting AP in foods, and for treatment or prevention of peanut allergy. (Updated on 11-SEP-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GCAACAGGAGCAACAGTICAAGAGGGAGCTCAGGAACTIGCCTCAACAGTGCGGCCTTAG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 GCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCCTCTCAGCACCAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGAGGCGCTGG
                                                                                                          transgenic peanut plants that produce allergen-free seeds, non-allergenic foods, by antisense or sense co-suppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 64.4%; Score 462; DB 4; Length 1162; Best Local Similarity 100.0%; Pred. No. 7.8e-111; Matches 462; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1162 BP; 272 A; 325 C; 329 G; 236 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 GGCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 2; 72pp; English.
                                                                                                              Producing transgenic peanut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF90342 standard; DNA; 80
                                                                                                                                                                              allergen-encoding genes
WPI; 2001-355630/37.
P-PSDB; AAB82383.
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This sequence represents the coding sequence for soybean albumin 3. This sequence represents a DNA molecule of the invention. The DNA molecules of the invention comprise a preselected DNA segment encoding a seed storage protein (SSP). (I) is used to produce transgenic seeds and plants, especially soybean plants that have increased levels of lysine and also increased levels of methionine and/or cysteine in albumin protein type 1 and/or 3. Increasing the levels of these amino acids increases the nutritional value of soybean produced. This is especially useful for producing animal feeds. The amount of lysine in the seed is increased by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Increasing the nutritional quality of soybean - by genetically increasing the amount of lysine, methionine and/or cysteine in albumin proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 GGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAGGCCCTG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 AAAAGACGAAGAAGAAGAAGAAGACACATGCAGAAGTGCTGCACAGAAATGAGCGA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCCACGCATCTGCGAGGCAGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 cacaarcerecrearerererererereseareseeeeerreseegeeereeaaars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 gcagcaccagcaaga---ragcreccecaagcagcrecagegegegegegecere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 CGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGACCCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 CGAGAAGCACATCATGGAGAAGATCCAAGGCCGCGGGGGATGACGATGATGATGATGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AGGCGCTGGATCCTCTCAGCACGAGAGGGTGTTGCAATGAGCTGAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5-10 %, the amount of methionine and cysteine is increased by 10-30%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 CAGC----CCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.1%; Score 65.6; DB 2; Length 777; 50.8%; Pred. No. 8.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 777 BP; 253 A; 161 C; 196 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                            /*tag= d
/note= "small chain coding sequence"
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/note= "large chain coding sequence"
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/note= "prepropeptide"
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 46-47; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC
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Best Local Similarity 50.8<sup>3</sup>
Matches 363; Conservative
                                                                            . 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-480228/44.
P-PSDB; AAW23419.
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     Glycine max
                                                                                                                           sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotides 11-91 of a published peanut allergen Ara h2 cDNA sequence.

The probe was used to screen a peanut genomic library for the isolation of the Ara h2 gene (see AAF90136). The invention relates to a method for producing a peanut plant having reduced, or undetectable, allergenic protein (AP) content in its seed. A peanut plant cell is transformed with a DNA construct containing an antisense AP gene and/or sense AP gene, or their fragments, regenerated to plants, and fertile transgenic plants that produce seeds with reduced AP content are identified. The AP sense or antisense gene may comprise at least a portion of the present sequence. The seeds are useful for preparation of allergen-free foods. Recombinant AP may be produced and used to produce antibodies useful for detecting AP in foods, and for treatment or prevention of peanut allergy. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of an oligonucleotide probe corresponding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing transgenic peanut plants that produce allergen-free seeds, useful in non-allergenic foods, by antisense or sense co-suppression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCCACGCATGCGAGGCAGCAGCAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCCACGCATCTGCGAGGCAGCAGTGGGAA
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0
                                                                                                                                                Peanut; allergen; Ara h2; transgenic plant; allergy; probe; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 80 BP; 17 A; 27 C; 21 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80; DB 4; Le
Pred. No. 5.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.2%; Scott No. 0. 100.0%; Pred. No. 0. 0. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viquez OM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean albumin 3 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 44; 72pp; English.
                                                                                              Peanut allergen Ara h2 gene probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konan KN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 CTCCAAGGAGACAGATG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCAAGGAGACAGAAGATG 80
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                                                                                                                                                                                                                                                                                                                                                                                                        99US-0167255P
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYAL-) UNIV ALABAMA A & M.
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergen-encoding genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arntzen CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-355630/37
                                                                                                                                                                                             Arachis hypogaea
                                                                                                                                                                                                                                                    WO200136621-A2
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                     11-SEP-2003
23-JUL-2001
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                                                                                                                                                                                                                                                                                                    25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dodo HW,
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molecule of the invention. The DNA molecules of the invention comprise a preselected DNA segment encoding a seed storage protein (SSP). (I) is used to produce transgenic seeds and plants, especially soybean plants that have increased levels of lysine and also increased levels of methionine and/or cysteine in albumin protein type 1 and/or 3. Increasing the levels of these amino acids increases the nutritional value of soybean produced. This is especially useful for producing animal feeds. The amount of lysine in the seed is increased by 5·10 %, the amount of methionine and cysteine is increased by 10·30%
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                                                                                                                                                                                             Length 777;
                                                                                                                                                              Sequence 777 BP; 253 A; 157 C; 197 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                            Query Match 8.9%; Score 64; DB 2; Length 777 Best Local Similarity 50.7%; Pred. No. 2.2e-06; Matches 362; Conservative 0; Mismatches 310; Indels
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                                                                                                                                                                             TACTATGTGCAGGTTTGGACCCATGATCCAGTGCGACTTGTCCTCCGA-----TGACTA 503
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                  GTTTGAGAACAACCAAAGGTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAG
                                   CGAGGAACTIGGAGGAGAAGAAGAAA---ATGGAGAAGGAGCTCATTAACTTGGC
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plant; animal feed production; chimeric protein;
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P-PSDB; AAW23420.
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transgenic soybean
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Glycine max.
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the amount
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This is the nucleotide sequence of a 770 bp portion of an isolated CDNA clone that codes for a soybean cotyledon-specific protein, termed Gm25-1 (see AAV05723). The CDNA was isolated in a search for sulphur-rich proteins in soybean seed. A CDNA library was prepared using polyA RNA from mid-maturation seed of soybean cv. Hodgson 78 and subjected to a RACE protocol using primers based on an N-terminal peptide of the curifical protein. The complete cDNA codes for a protein having a 21-amino acid residue signal peptide and a pro-protein that is post.

CHUMSAIN) with a unique C-terminal end containing the RGD cell adhesion motif followed by 8 Asp residues, a 17-amino acid linker peptide, and a 77 amino acid (8 kDa) large subunit (alisin) that is rich in sulphur contains in 19sine (13.0%) and cysteine (7.8% methionine) in 19sine (13.0%) and cysteine (7.8% protocol peptide, protein a target cell, including mammalian, plant and bacterial colls, in vitro or in situ. The methods involve contacting the cell with a nucleic acid encoding the peptide, particularly a lunasin and/or alisin peptide. The peptide modulates expression of a resident Gm25-1 peptide-encoding contranscript. The invention also encompasses nucleic acid hybridisation probes and primers for use in identifying, cloning, compliance or transcript. The invention also encompasses nucleic acid muplifying and/or medulating the expression of a resident Gm25-1 peptide-encoding contacting the modulating the expression of a modulating the expression of a dem25-1 peptide-encoding conspiration of modulating the expression of a dem25-1 peptide cell demandating the expression of a dem25-1 peptide cell demandating the expression of a modulating the expression of a dem25-1 peptide cell demandating the expression of a dem25-1 peptide cell demandating the expression of a dem25-1 peptide cell demandating the expression of a dem25-
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                                        lunasin, alisin, soybean, albumin, cotyledon, mitosis, disruptor; cancer, restenosis; therapy, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63.4; DB 2; Length 770;
Pred. No. 3.1e-06;
0; Mismatches 301; Indels 4
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                                                                                                                                                 Location/Qualifiers
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51.6%;
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P-PSDB; AAY05723.
Soybean Gm2S-1 cDNA
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Matches 369; Conserv
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                                                                                                          205 CGACAATCACATTCTCAGGACCATGCGGGGAAGAATCAACTACATAAGGAGGAACGAAGG
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AJ498204 sc91g03.y sf90d06.y sg60e10.y sg61b03.y sg62c02.y sg72b07.y

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sg73h12.y sg71d12.y sb62h10.y su74e01.y

Scoring table:

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Minimum DB Maximum DB

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Run on:

8974908.y 8964c10.y 8967d07.y

sg79f01.y su72c09.y sb48a09.y sg78a09.y

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Arachis hypogaea (peanut)

EMARCHIS Hypogaea

EMARYOCATE, VITIGUEJANTAE; EMBRYOPHYTA; Tracheophyta;

EMARYOCATE, VITIGUEJANTAE; ENGIGOTYJEGONS;

COSIGS; eurosids I; Fabales; Fabaceae; Papilionoideae;

Aschynomeneae; Arachis.

I (bases 1 to 788)

E 1 (bases 1 to 788)

Luo, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G. and Lynch, R.E.

Generation and Analyses of ESTs for Arachis hypogaea

Unpublished (2003)

Contact: Baozhu Guo

Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd., Tifton, GA 31794, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear EST 07-MAY-2003
Pod cDNA Library (UTPP)
5', mRNA sequence.
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CO897509 E
CN825259 I
CD038103 U
BF594963 E
BE661358 4
BE658140 C
                                                                                                                     AJ498204
AN2780869
AW318110
AW318110
AW318110
AW395515
AW395515
AW395515
AW395679
AW395679
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/clone="UTPP1007_C04"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_hoste:"XL1-blue"
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/organism="Arachis hypogaea"
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AW318155
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Email: bguo@tifton.usda.gov
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/cultivar="A13"
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ORGANISM
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JOURNAL
COMMENT
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CD038313 UTPP1006
CD038323 UTPP1005
CD038459 UTPP1005
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CD038459 UTPP1005
CD038415 UTPP1006
CD038334 UTPP1006
CD03834 UTPP1006
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CZ55065 02SQ16-0
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CD038092 UTPP1002
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CD038861 UTPP1002
DT9566 EST000012
CD038841 UTPP1002
DT9566 UTPP1004
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                                                                                                                 June 23, 2006, 09:32:31 ; Search time 3685.01 Seconds (without alignments) 10880.347 Million cell updates/sec
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              GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Maximum Match 100%
Listing first 45 summaries
                                                                                nucleic search, using sw model
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29.1
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118.1
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666 555.2 487.8 315.2 283.8 223.8 223.8 147.8 1133.4 1133.5 1133.6 1131.8 86

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Score

Result

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and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was islamed with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Unic.ZAP, XR vector using XhoI
                                                                                                                                                                                                              ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG 449
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/ucce="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; CDNA library was constructed from peanut cultivar Al3 (NCV11XARA). Al3 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 50bb were collected after size-fraction. The inserts were directionally cloned into Uni.ZAP XR vector using XhoI EcoRI sites adapters. The landa library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to extise plauescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
CD038213 689 bp mRNA linear EST 07-MAY-2003 UTPPI004_A09 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPPI004_A09 5', mRNA sequence.
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                                                                                                                                                                                                 Arachis hypogaea
Bukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
                                                                                                                                                                                                                                                                                                                                                                Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GACGAGGATTCATATGAACGGGACCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 CAGCTCGAGAGGGGGAACCTGAGGCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 GCTGCCCACGCATCTGCGAGGCAGCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2321
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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llarity 99.6%; Pred. No. 8e-155;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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/clone="UTPP1004_A09"
/tissue_type="Immature pods"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arachis hypogaea"
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/lab_host="XL1-blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="A13"
                                                                                                                                                                       Arachis hypogaea (peanut)
                                                                                                                                                                                                                                                                                                            Aeschynomeneae; Arachis.
                                                                                                                CD038213.1 GI:30420051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: T3.
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nes 677; Conserv
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/OCCE="Vector: Uni-ZAP XR; Site 1: ECORI; Site 2: Xhol; CDNA library was constructed from peanut cultivar Al3 (NCV1XARA). Al3 has resistance to Appergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in .80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGCAATGAGCTGAACGAGTTTGAGAACAACCAAAGGTGCATGTGCGAGGCATTGCAACA 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGGATCCTCTCAGCACCAAGAGAGGTG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAGGTGCATGTGCGAGGCATTGCAACA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAGGCAACAGGAGCAACAGTTCAAGAG 384
  /lab_host="XL1-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 GCCCTGCGAGCAACATCTCATGCAGAAAATCCAACGTGACGAGGATTCATATGGACGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.4%; Score 555.2; DB 4; Length 732; 93.1%; Pred. No. 3.3e-127; ive 0; Mismatches 9; Indels 37
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Best Local Similarity 93.19
Matches 617; Conservative
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                       TTGCCTCAACAGTGCGGCCTTAGGGCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGC 420
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Mkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae;
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Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
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'94, USA
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/mol_type="mRNA"
/cultivar="A13"
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/clone="UTPP1006_E02"
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USDA/ARS, Crop Protection ar
2747 Davis RG., Tifton, GA 7
Tel: 229-387-2334
Fax: 229-387-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: bguo@tifton.usda.gov
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1 (bases 1 to 732)
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UTPP1005_F05 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPP1005_F05 5', mRNA sequence.
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Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosida I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
361 GTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAGGGCACCACAGCGTTG 420
                                                                                                                      /clone lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
                                                               Generation and Analyses of ESTs for Arachis hypogaea Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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                                                                                                                                                                                   496 AAAGAAAAGAAAATAGCTTATATATAAGCTATTATCTAT 539
                                                                                                                                                                                                                   tissue type="Immature pods"
/dev stage="R6"
/lab_host="XL1-blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arachis hypogaea"
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/clone="UTPP1005_F05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/cultivar="A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD038323.1 GI:30420161
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91.1%;
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CD038323
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                                                                                                                                                                                                                   CO897505 524 bp mRNA linear EST 13-AUG-2004 EST00010 Peanut Lambda Express library Arachis hypogaea cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAGGGCACCACAGCGTTG 435
                                                                                                                                                                                                                                                                                                                                                                                                                               Arachis hypogaea
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids 1; Pabales, Fabaceae, Papilionoideae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGGGGCGCTGGATCCTCTCAGCACCA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAGGTGCATGTGCGAGGC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAGGCAACAGGAGCAACA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: Shangzhi Huang
Contact: Shangzhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology
GuangZhou, 510275, China
Tel: (860)02084036592
Email: yys880304yahoo.com.cn
Seq primer: pTriplEx2 Forward.
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I (bases 1 to 524)
Yan, Y.S., Wang, L. Zhong, Y.J. and Huang, S.Z.
Expressed sequence tags of mid-matured cotyledons of peanut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3818"
/tissue_type="Cotyledons"
/dev_stage="Mid-matured stage"
/lab_host="Ecoli BM25.8"
/clone_lib="Peanut Lambda Express library"
/note="Organ: Seed; Vector: lambdaTriplEx2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .524
/organism="Arachis hypogaea"
/mol type="mRNA"
/cultivar="Yueyou 523"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         Arachis hypogaea (peanut)
                                                                                                                                                                                                                                                                                                                                            CO897505.1 GI:51237295
                                                                                                                                                                                                                                                                                      mRNA sequence.
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729 AGC
   AGC
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(UVIPP) (UVIPP) (UVIPP) (UVIPP) (UVIPP) (UVIPP) (UVIPP) (UVIPP) (UVIPP) (UVIVINAR4) as constructed from peanut cultivar All (NOVINAR4) all has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (SIBCOBR). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and ilbrary construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise plausescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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Pod cDNA Library (UTPP)
5', mRNA sequence.
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                                                                                                                                                                        /dev_stage="R6"
/lab_host="XII-blue"
/clone lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 CATCACTATATGAATGTGTTGATCGTGTTAACTAAGGCAAGCTTAGGTTATATGAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%; Score 315; DB 4;
ilarity 99.7%; Pred. No. 2.1e-67;
Conservative 0; Mismatches 0
                                                                          /mol_type="mRNA"
/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPP1005_D03"
/tissue_type="Immature pods"
                                                          /organism="Arachis hypogaea"
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                    location/Qualifiers
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Arachis hypogaea
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CD038459.1 GI:30420297
    Seq primer: T3
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Matches 326; Conserv
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    ë,
                                                                                                                                      TATGATCGGAGAGGCGCTGGATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAC 180
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                                                                                                                  ------GATCCGTACAGCCCTAGTCCA 220
                                                                                                                                                                                          TATGATCGGAGGGCGCTGGATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAC 280
                                                                                                                                                                                                                                                                    GAGTTTGAGAACAACCAAAGGTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAG 340
                                                                                                                                                                                                                                                                                                                                                AGCGATAGGTTGCAGGGGAGGCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTG 400
                                                                                                                                                                                                                                                                                                                                                                          CCTCAACAGTGCGGCCTTAAGGGCACCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCAACAGTGCGGCCTCAGGGCACCACAGCGTTGCGACTTGGAAGTCGAAAGTGGCGGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAATGTGTTGATCGTGTTAACTAAGGCAAGCTTANGTTATATGAGCACCTTTAGAGTGC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATATAAGCTATTATCTATGGTTATGTTTTAGTAATAATAAAGATCATCACTATA 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATATAAGCTATTATCTATGGTAATG-TTAGTTTTTGGTAATAATAAAGATCATCACTATA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTT--AIGGCGTIGTCTAIGTTTTGTIGCTGCAGAGTIGTAACCAICTTGAAAIAATAI 698
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Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Pabalee, Fabaceae, Papilionoideae,
                                                          1 CTCATGCAGAAAATCCAACGTGACGAGGATTCATATGGACGGGACCGGTACAGCCCTAGT 60
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Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
and Lynch,R.E.
                                                                                                                                                                                                                                                                                            GAGTTTGAGAACAACCAAAGGTGCATGTGCGAGGCATTGCAACAGATAATGGAGAAACCAG
                                      CTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGACCCGTACAGCCCTAGT
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    Gaps
    39;
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USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd. Tifton, GA 31794, USA
TE1: 229-387-2334
Fax: 229-387-2321
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Contact: Baozhu Guo
  16; Indels
Mismatches
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Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 GGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAGGGCACC 426
                                                                                                                                                                           CO897504
EST00009 Peanut Lambda Express library Arachis hypogaea cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: ShangZhi Huang plant Diology plant Development and Molecular Biology plant Davelopment and Molecular Biology and Biotechnology Sun Yat-sen University, Department of Biology and Biotechnology GuangZhou, 510275, China Tel: (860)02084036592 Email: yys9803@yahoo.com.cn Seq primer: pTriplEx2 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TCAGCACCAGGAGGGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAGGTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 CGAGAGGGCGAACCTGAGGCCCTGCGAGCAACATCTCATGCAGAAGATCCAAGGTGACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 cgagaggggggaacctraggcccrgcgagcaacarcrcargcagaaarccaacgrgacga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Yueyou 523"
/db xref="texon:3918"
/tissue_type="Cotyledons"
/dev stage="Mid-matured stage"
/lab_host="E.coli BM25.8"
/clone lib="Peant Lambda Express library"
/note="Organ: Seed; Vector: lambdaTriplEx2"
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llarity 88.8%; Pred. No. 1.5e-59;
Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GGATTCATATGAACGGGACCCGTACAGCCCTAGTCAG
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/organism="Arachis hypogaea"
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CO897504
CO897504.1 GI:51237294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UVIPP) (VOICE="Vector: Uni-ZAP XR; Site 1: ECORI; Site 2: XhOI; CDNA library was constructed from peanut cultivar Al3 (NCVIIXAR4). Al3 has resistance to Appergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). CDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamma library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
                                                                                                             Bausher, M.G.
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                                                                                                                                                                       Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
40.3%; Score 289; DB 4; Length 308;
Best Local Similarity 99.7%; Pred. No. 6e-61;
Matches 300; Conservative 0; Mismatches 0; Indels
                                                                                                                                                           Generation and Analyses of ESTs for Arachis hypogaea
                                                                                                             Lee, R.D.,
                                                                                                        Luo, M., Dang, P., Guo, B. Z., Holbrook, C.C., and Lynch, R.E.
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/lab_host="XL1-blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="Al3"
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/clone="UTPP1007 F09"
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                                                                                                                                                                                                                                                                                                                        Fax: 229-387-2321
Email: bguo@tifton.usda.gov
                                                                Aeschynomeneae; Arachis.
1 (bases 1 to 308)
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DEFINITION

RESULT 9 CD038415

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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CD038394 132 bp mRNA linear EST 07-MAY-2003 UTPP1006_F02 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPP1006_F02 5', mRNA sequence.
  518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      626 GCTCTTATGGCTTTACCTGTGTTTTTGCTACTGCAAAGTTTTTAACCACCACCATGAAAAAAG 685
                                                                                                                                                                                         399 IGCCTCAACAGIGCGGCCTTAGGGCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCG 458
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosida, eurosida I, Fabales, Fabaceae, Papilionoideae,
Aeschynomeneae, Arachis.
1 (bases 1 to 732)
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                                                                                                                                       519 TATATATAAAGCTATTATCTATGGTTATGTTTTGGTAATAATAAAGATCATCACTA
                                                                                                                                                                                                                                                                                               and Lynch, R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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/dev_stage="R6"
/lab_host="XL1-blue"
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/organism="Arachis hypogaea"
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/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPP1006_F02"
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CDNA library was constructed from peanut cultivar Al3
(NCVIIXARA). Al3 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIZOL-Reagent
ultrapure (GIRCORN). mRNA was extracted and purified from
total RNA (Promega). CDNA synthesis and library
construction followed the protocol of by ZAP-CDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
ECORI sites adapters. The lamda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector. and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
                                                                                                                                                          CD038415 696 bp mRNA linear EST 07-MAY-2003
UTPP1006_H11 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPP1006_H11 5', mRNA sequence.
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Arachis hypogaea (peanut)
Bukaryota, Wiridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; endicotyledons; core eudicotyledons; cosida; eurosida I; Rabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and Analyses of ESTs for Arachis hypogaea Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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/dev_stage="R6"
/lab_host="XL1-blue"
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/cultivar="A13"
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                                    (bases 1 to 661)
,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
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                                                                                                                                                                           Contact: Baozhu Guo
Molecular Genetica
USDA/ARS, Crop Protection and Management 1
2747 Davis Rd., Tifton, GA 31794, USA
181: 229-387-2331
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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/lab_host="XL1-blue"
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Generation and Analyses of
Unpublished (2003)
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'cultivar="A13"
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ACVIIXAR4). Al3 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to Re stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). CDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The landal library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector. and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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Arachis hypogaea cDNA clone UTPPI005_F10 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 215.2; DB 4; Length 7 Pred. No. 1.7e-42; 0; Mismatches 108; Indels
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Arachis hypogaea
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Best Local Similarity 72.0%;
Matches 347; Conservative
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 bp mRNA linear EST 13-AUG-200
EST000013 Peanut Lambda Express library Arachis hypogaea cDNA 5',
CO897508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 TAATGGAGAACCAGTGCGATAGGTTGCAGGACAGGCAAATGGTGCAGCAGTTCAAGAGAG 130
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                                                                                                                                                                                                                                        Biology and Biotechnology
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Yan, Y.S., Wang, L., Zhong, Y.J. and Huang, S.Z.
Expressed sequence tags of mid-matured cotyledons of
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                                          Indels
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llarity 83.9%; Pred. No. 1.1e-24;.
Conservative 0; Mismatches 31;
       Pred. No. 8.9e-26;
0; Mismatches 7;
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Context: Shangzhi Huang
Plant Development and Molecular Biology
Ruangzhou, 510275, China
Tel: (860)02084036592
Email: Yy980108yahoo.com.cn
Seq primer: pTriplEx2 Forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arachis hypogaea"
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   94.98;
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   Local Similarity 94.9
nes 185; Conservative
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Arachis hypogaea
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Best Local Similarity
Matches 162; Conserv
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                                      Matches
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CO897508
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/note="Vector: ToPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
                                                                                                                                                                                                                                        403 CAGGGCACCACAGCGTTGCGATTTGGACGT-----GAGTGGCGGCAGATGCTAGAC 453
                                                                                                                                                                                                                                                                                                                                                                                                              513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTTATGTTTAGTTTTGGTAATAATAAGATCATCACTATATGAATGTGTTGATCGTG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 TTAACTAAGGCAAGCTTAGGTTATATGAGCACCTTTAGAGTGCTTTTATGGCGTTGTCTA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 GAGATGCATGTGCGAGGCATTGCAGCAGATAATGGAGAACCAGTGCGATAGGTTGCAGGA 342
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CZS50656 1nnear GSS 24-MAY-20
0280166-05A1-H01 UniformMu MuTAIL Library Zea mays genomic clone
0280166-05A1-H01, genomic survey sequence.
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                                                                   GAGGCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCT
                                                                                                                                  343 CAGGCAAATGGTGCAGCAGTTCAAGAGAGCTCATGAACTTGCCTCAACAGTGTAACTT
                                                                                                                                                                                                  TAGGGCACCACAGGGTTGCGACTTGGACGTCGAAAGTGGCGGCAGAGACAGATACTAAAC
                                                                                                                                                                                                                                                                                                                                        454 TCAAAAATAATAATCTGTGCCAAAAGAACTAGTAGGAAGTAGCTTATGAGCTATTATGT
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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Contact: Donald R. McCarty
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drm@ufl.edu
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/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
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/clone="0280166-05A1-H01"
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Zea mays
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LOCUS DEFINITION

ACCESSION

RESULT 12 CZ550656/c

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

source

ORIGIN

FEATURES

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316 ATTGCAACAGATCATGGAGAACCAGAGCGATAGGTT---GCAGGGGAGGCAACAGGAGCA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.6%; Score 133.2; DB 4;
Best Local Similarity 58.3%; Pred. No. 4.4e-22;
Matches 344; Conservative 0; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arachis hypogaea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:3818"
/clone="UTPP1002_D04"
/tissue_type="Immature pods"
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="A13"
                                                                                                                                                                                                                                                                                                                                                                                                    . .680
                                                                                                                                                                                                                                                                                                                                                                Seq primer: T3.
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                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                            CO897506 286 bp mRNA linear EST 13-AUG-2004
EST000011 Peanut Lambda Express library Arachis hypogaea cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                               Asschynomeneae; Arachis, Land Huang, Land, Land Huang, Land, Land Huang, L. Zhong, Y. J. and Huang, S. Z. S. Yan, Y. S., Wang, L., Zhong, Y. J. and Huang, S. Z. Expressed sequence tags of mid-matured cotyledons of peanut Unpublished (2004)

L. Unpublished (2004)

Contact: ShangZhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology GuangZhou, 510275, China
Tel: (860)02084036592

Email: yys9803@yahoo.com.cn
Seq primer: pTriplEx2 Forward.
Seq primer: pTriplEx2 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 ACGAGATGGAGAACACACAGAGATGCATGTGCGAGGCATTGCAGCAGATAATGGAGAACC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AGAGCGATAGCTTGCAGGGGAGGCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACT 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Peanut Lambda Express library"
/note="Organ: Seed, Vector: lambdaTriplEx2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Yueyou 523"
/db_xref="taxon:3818"
/tissue_type="Cotyledons"
/dev_stage="Mid-matured stage"
/lab_host="E.coli BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Arachis hypogaea"
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EST.
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                       447 TCGAAAGTGGCGG 459
                                                         191 reagredecécea 203
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                                                                                                                                                                                                                                                                                                         Arachis hypogaea
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Arachis hypogaea (peanut)
Arachis hypogaea
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 TCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGGATCCTCTCAGCACCA 255
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/lab_host="XL1-blue"
/clone lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 680)
Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
and Lynch,R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 cataalgechaalgestegagechaelaechaeleenaalgechaeleaechaeleena
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and Analyses of ESTs for Arachis hypogaea Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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Sequence 1, Appli
Sequence 14, Appli
Sequence 1777, Appli
Sequence 1777, Appli
Sequence 18554, A Sequence 16554, A Sequence 16554, A Sequence 16554, A Sequence 1, Appli
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Sequence 6, Appli
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Sequence 9, P
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Sequence 3, P
Sequence 1, P
Sequence 1, P
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-191-593-6
US-09-191-593-9
US-09-106-872A-1
US-09-715-036-1
US-09-715-036-1
US-08-618-911-3
US-08-618-911-5
US-08-618-911-5
US-08-618-911-5
US-08-938-675A-1
US-08-938-675A-1
US-08-938-675A-1
US-08-938-675A-1
US-08-948-0715-036-8
US-08-948-016-10205
US-09-949-016-10205
US-09-949-016-10205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1403666 segs, 935554401 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              - nucleic search, using sw model
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seq length: 200000000
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Perfect score:
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80
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                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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No.
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Sequence 11892, A Sequence 17296, A Sequence 17296, A Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 15425, A Sequence 20, Appl Sequence 20, Appl Sequence 1576, A Sequence 1576, A Sequence 1576, A Sequence 1576, A Sequence 15676, A Sequence 15676, A Sequence 151214, A Sequence 151214, A Sequence 1511, A Sequence		Length 717; Indels 0; Gaps 0; GCCCACGCATCTGCGAGGCA 60 GCCCACGCATCTGCGAGGCA 60 GCCCACGCATCTGCGAGGCA 60 GCCCAGGAGGGCGAACCTGAG 120 CTCGAGAGGGCGAACCTGAG 120 GAGGATTCATATGAACGGGA 180 TATGATCGGAGAGGCGCTGG 240 INIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
US-09-949-016-11892 US-09-949-016-17296 US-09-949-016-11973 US-09-949-016-15824 US-09-244-796-17 US-09-244-796-17 US-09-28-502-1 US-09-28-502-1 US-09-87-211-1 US-09-949-016-16807 US-09-949-016-16807 US-09-949-016-16807 US-09-106-872A-2 US-09-106-872A-1 US-09-106-872A-1 US-09-106-872A-1 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576 US-09-949-016-1576	ALIGNMENTS 09106872A 681ey ven Allergens and Methods US/09/106,872A 06-29 PCT/US96/15222	DB 3; es 0; crccrcccr CTCCTCCCTCCCT CTCCTCCCTCCCTCCCTCCCTCCC
6 6.0 251672 3 4 5 5.0 135182 3 4 5 5.0 135182 3 3 2 2 5 5 9 5 630 2 2 5 5 9 197452 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 8 6 2873 3 5 6 5 6 5 8 6 2873 3 5 6 6 5 8 6 5	Application US/ 86311 Burks Jr., A. W Stanley, J. Ste Cockrell, Gael King, Nina E. Sampson, Hugh A Helm, Ricki M. Bannon, Gary A. VENTION: Peanut VENTION: Peanut VENTION: Peanut NGE: HS 103 CIP ING DATE: 1999- ATTION NUMBER: CATTON NUMBER:	Similarity 100.0%; Score 717; Similarity 100.0%; Pred. No. 77; Conservative 0; Mismatch GCTCACCATACTAGTAGCCCTCGCCTTTTC GCTCACCATACTAGTAGCCCTCGCCTTTTC GCAGTGGGAACTCCAGGAGACAGAGATCCAGGAGACACACTCATGCAGAGATCCCTGCCTTTTC GCCGTACAGGAACATCTCATGCAGAAGATCCCTGCCGGAGAACATCTCATGCAGAAGATCCCTGCCGAGCAACATCTCATGCAGAAGATCCCCTAGCAGAACATCCCTAGCAGAAGATCCCCTAGCAGAACATCTCATGCAGAAGATCCCCTAGCAGAACACTCTCATGCAGAAGATCCCCTAGCAGAACACCCCTAGTAGAACACTCTCATGCAGAAGATCCCCTAGTAGAACACTCTCATGCAGAACACTCCCTAGTACAGAACCCCTAGTACAGACCCTAGTACAGACCCTAGTACAGACCCTAGTACAGACCCTAGTACAGATCCGTACAGCCCTAGTACAGCACCCTAGTACAGGATCCGTACAGCCCTAGTACAGCCCTAGTACAGCCCTACAGCCCTAGTACAGCACCCTAGTACAGCACCCTAGTACAGCCCTAGTACAGCCCTACAGCCCTAGTACAGCCCTACAGCCCTAGTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACAGCCCTACACACCAC
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-106-872A Sequence 20, Retent No. 6, RESERAL INFO APPLICANT: AP	

US-08-916-421B-1 US-09-692-570-1 US-09-949-016-14026 US-09-949-016-16226 US-09-949-016-13004

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                                                                                            301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG 360
                                                                                                                                                                                           GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAG 420
                                                                                                                                                                                                                                           361 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAG 420
                                                                                                                                                                                                                                                                                               GGCACCACAGGGTTGCGACTTGGACGTCGAAAGTGGCGGCAGAGACAGGATACTAAACACC 480
                                                                                                                                                                                                                                                                                                                                             421 GGCACCACAGAGGTTGCGACTTGGACGTCGAAAGTGGCGGCAGAGAGACAGATACTAAACACC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTAAGGCAAGCTTAGGTTATATGAGCACCTTTAGAGTGCTTTTATGGCGTTGTCTATGT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 ACTAAGGCAAGCTTAGGTTATATGAGCACCTTTAGAGTGCTTTTATGGCGTTGTTGTT 660
241 ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACAAAG 300
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                                                                                                                             301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGGG
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APPLICANT: BIRKS, A Wesley, HELM, Ricki M,
APPLICANT: BIRKS, A Wesley, HELM, Ricki M,
APPLICANT: BIRKS, A Wesley, HELM, Ricki M,
APPLICANT: BANNON, Gary A
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Head, Johnson & Kachigian
STREET: 112 W. Center St., Suite 230
CITY: Fayetteville
STATE: Arkansas AR
COUNTRY: United States of America
ZIP: 72701
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb
MEDIUM TYPE: Bistorage
COMPUTER READABLE FORM:
MEDIUM TYPE: UNIVERSE 1998
COMPUTER STATES
SOFTWARE: WORDSEE 1998
COMPUTER: 13 NOVEMBER 1998
FILING DATE: 13 NOVEMBER 1996
APPLICATION NUMBER: US 07/998, 377
FILING DATE: 30 BECEMBER 1995
APPLICATION NUMBER: US 08/717, 933
FILING DATE: 29 SECEMBER 1995
APPLICATION NUMBER: US 08/717, 933
FILING DATE: 29 DECEMBER 1995
APPLICATION NUMBER: US 08/124
FILING DATE: 29 DECEMBER 1995
APPLICATION NUMBER: US 08/610,424
FILING DATE: 04 MARCH 1996
ATTORNEY/AGENT INFORMATION:
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Patent No. 6835824
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US-09-191-593-6
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100.0%; Score 717; DB 3; Length 717;
Best Local Similarity 100.0%; Pred. No. 1.1e-185;
Matches 717; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHROMOSONE/SEGNETT: No. 6835824 applicable
MAP POSITION: No. 6835824 applicable
UNITS: No. 6835824 applicable
UNITS: No. 6835824 applicable
FRATURE:
NAME/KEY: CDS
LOCATION: 2.475
LDENTIFICATION METHOD: By agreement with
IDENTIFICATION METHOD: protein information and
CTHER INFORMATION: Seed storage protein and
OTHER INFORMATION: allergen
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
TITLE:
TITLE:
COURNAL:
NAME: ALEXANDER, DANIEL R
REGISTRATION NUMBER: 32,604
REFERENCE/DOCKET NUMBER: ARK00895601B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (501) 582-9111
TELEFAX: (501) 521-4931
TELEX: No. 6835824 applicable
INFORMATION FOR ENG ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: Florunner seed cDNA expression
LIBRARY: library in Uni-ZAP XR vector
CLONE: P38
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA to mRNA
DESCRIPTION: identified as Ara h II P38
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: Clone P38
DEVELOPRENTAL STAGE: Seed
THEOTYPE: No. 635824 applicable
TISSUE TYPE: Seed mRNA, cDNA library
CELL IYPE: No. 6835824 applicable
ORGANELLE: No. 6835824 applicable
ORGANELLE: No. 6835824 applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: No. 6835824 applicable ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arachis hypogaea
                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arachis
STRAIN: Florunner
                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD: By agreement with IDENTIFICATION METHOD: protein information and established IDENTIFICATION METHOD: consensus sequence OTHER INFORMATION: Seed storage protein and OTHER INFORMATION: allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 717; DB 3; Length 717; Best Local Similarity 100.0%; Pred. No. 1.1e-185; Matches 717; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: identified as Ara h II cDNA clone
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No. 6835824 applicable
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMOSOME/SEGMENT: No. 6835824 applicable MAP POSITION: No. 6835824 applicable UNITS: No. 6835824 applicable
             FILING DATE: 29 DECEMBER 1995
APPLICATION NUMBER: US 08/610,424
FILING DATE: 04 MARCH 1996
ATTORNEY/AGENT INFORMATION:
NAME: ALEXANDER, DANIEL R
REGISTRATION NUMBER: 32,604
REFERENCE/DOCKET NUMBER: ARK00895601B
TELECOMMUNICATION INFORMATION:
TELEPRAN: (501) 582-9111
TELEFRAX: (501) 582-9111
TELEFRAX: No. 6835824 applicable
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: florunner seed cDNA expression
LIBRARY: library in Uni-ZAP XR vector
CLONE:
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: Florunner
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: seed
HAPLOTYPE: No. 6835824 applicable
TISSUE TYPE: No. 6835824 applicable
CELL LINE: No. 6835824 applicable
OKGANELLE: No. 6835824 applicable
OKGANELLE: No. 6835824 applicable
IMMEDIATE SOURCE:
US 60/009,455
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                           717 nucleotides
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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VOLUME:
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                                          ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAG 300
                                                                                                                                                                                                                                                     GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCAGAGACAGATACTAAACACC 480
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US-09-191-593-9

Sequence 9, Application US/09191593

Sequence 9, Application US/09191593

Sequence 9, Application US/09191593

Sequence 9, Application US/09191593

PERET NO. 6835824

APPLICANT: BURKS, A Wesley, HELM, Ricki M, APPLICANT: COCKRELL, Gael, STANLEY, J Steven, APPLICANT: BANNON, Gary A TITLE OF INVENTION: PEANUT ALLERGENS AND STREET: 112 W. Center St., Suite 230

STREET: 112 W. Center St., Suite 230

CITY: Fayetteville STATES AREADABLE FORM: MRDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb MEDIUM TYPE: Wordperfect 6.0C

COMPUTER: Nordperfect 6.0C

COMPUTER: Nordperfect 6.0C

COURRENT APPLICATION NUMBER: US/09/191,593

FILING DATE: 13 NOVEMBER 1996

APPLICATION NUMBER: US 07/998,377

FILING DATE: 23 SEPFEMBER 1995

APPLICATION NUMBER: US 07/998,377

FILING DATE: 29 NOVEMBER 1993

APPLICATION NUMBER: US 08/1158,704

FILING DATE: 29 NOVEMBER 1993
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GCTCACCATACTAGTAGCCCTCGCCCTTTTTCCTCGCTGCCCACGCATCTGCGAGGCA
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Patent No. 6943010
GENERAL INFORMATION:
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CORGANISM: Arachis hypogaea
US-09-715-036-3
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US-09-715-036-3
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; Sequence 1, Application US/09106872A
; Sequence 1, Application US/09106872A
; APPLICANT: Burks Jr., A. Wesley
; APPLICANT: Stanley, J. Steven
; APPLICANT: Cockrell, Gael
; APPLICANT: Sampson, Hugh A.
; APPLICANT: Ming Nina E.
; APPLICANT: Helm, Ricki M.
; APPLICANT: Bannon, Gary A.
; TILLE OF INVENTION: Peanut Allergens and Methods
; FILE REFERENCE: HS 103 CIP
; CURRENT APPLICATION NUMBER: US/09/106,872A
; FILE REPERENCE: HS 103 CIP
; CURRENT FILING DATE: 1999-06-29
; PRIOR FILING DATE: 1996-09-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 1
; LEMGTH: 743
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US-09-106-872A-1
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APPLICANT: DODO, HORTENSE W.
APPLICANT: ARNIZEN, CHARLES J.
APPLICANT: KONAN, KOFFI N'DA
APPLICANT: WONAN, KOFFI N'DA
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: TRANSCENIC PEANUT SEEDS
TITLE OF INVENTION: TRANSCENIC PEANUT SEEDS
FILE REFERENCE: 07212/0104
CURRENT APPLICATION NUMBER: US/09/715,036
CURRENT FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTING OFFE: 1999-11-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTING OFFE: 2.1
SEQ ID NO 3
LENGTH: 682
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6 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGTCGCCCACGCATCTGCGAGGCA
                                                                           61 GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGGCCAGCTCGAGAGGGGGGAACCTGAG
                                                                                                     66 GCAGTGGGAACTCCAAGGAGAGAGAGATGCCAGAGCCAGCTCGAGAGGGGGAACCTGAG
                                                                                                                                                                                121 GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA
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178 GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGCGCGAACCTGAG 237
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APPLICANT: DODO, HORTENSE W.
APPLICANT: KONAN, KOPFI N'DA
APPLICANT: KONAN, KOPFI N'DA
APPLICANT: WOMEN, KOPFI N'DA
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: TRANSCRIC PEANUT SEEDS
FILE REFERENCE: 072121/0104
CURRENT FILING DATE: 2000-11-20
PRIOR PAPLICATION NUMBER: 60/167,255
PRIOR PAPLICATION NUMBER: 60/167,255
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 7
LENGTH: 80
                                                                                   238 GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGA
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Sequence 3, Application US/08618911
Patent No. S850016
GENERAL INFORMATION:
APPLICANT: Jung, Rudolf
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Sequence 1, Application US/09715036

Sequence 1, Application US/09715036

GENERAL INVORMATION:
APPLICANT: DODO, HORTENSE W.
APPLICANT: KOMAN, KOFFI N'DA
APPLICANT: KOMAN, KOFFI N'DA
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING
CURRENT APPLICATION NUMBER: US/09/715,036

CURRENT FILING DATE: 1299-11-19

NUMBER OF SEQ ID NOS: 8

SOOFWARR: PATCHING DATE: 2.1
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  64.4%; Score 462; DB 3; Length 682; 100.0%; Pred. No. 4.2e-116; ive 0; Mismatches 0; Indels
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                       Best Local Similarity 100.
Matches 462; Conservative
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LOCATION: (110)..(730)
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LENGTH: 1162
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US-09-715-036-1
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450 TACTATGTGCAGGTTTGGACCCATGATCCAGTGCGACTTGTCCTCCGA-----TGACTA 503
                                                                     504 AGAAGTTAAAAGCAATGTTGTCACTTGTACGTACTAACACATGATGTGATAGTTTATGCT
                                                                                                                                                            523 TATAAGCTATTATCTATGGTTATGTTTAGTTTTGGTAATAATAAGATCATCACTATATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jung, Rudolf
APPLICANT: Hastings, Craig
APPLICANT: Coughlan, Sean
APPLICANT: Hu, David
TITLE OF INVENTION: ALTERATION OF AMINO ACID COMPOSITIONS IN
TITLE OF INVENTION: SEEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 777;
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Pred. No. 1.9e-07;
0; Mismatches 310; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,911
FILING DATE: Concurrently herewith
ATTORNEY/AGENT INPORMATION:
NAME: Simon, Soma
REGISTRATION NUMBER: 35.444
REFERENCE/DOCKET NUMBER: 365-US
TELECOMMUNICATION:
TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: PIONEER HI-BRED INTERNATIONAL, INC 700 Capital Square, 400 Locust Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5850016
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ilarity 50.7%;
Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER H
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Best Local Similarity
Matches 362; Conserv
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LOCATION:
US-08-618-911-5
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                                       ALTERATION OF AMINO ACID COMPOSITIONS IN SEEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65.6; DB 2; Length 7'
Pred. No. 6.8e-08;
0; Mismatches 309; Indels
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                         ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/618,911
FILING DATE: Concurrently herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Simon, Soma
REGISTRATION NUMBER: 37,444
REFERENCE/DOCKET NUMBER: 365-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAK: (515) 248-4804
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
APPLICANT: Hastings, Craig
APPLICANT: Coughlan, Sean
APPLICANT: Hu, David
TITLE OF INVENTION: ALTERATI
TITLE OF INVENTION: SEEDS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 50.8
Matches 363; Conservative
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28..501
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MOLECULE TYPE:
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, LOCATION:
US-08-618-911-3
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REGISTRATION NUMBER: 36,627
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                                            GCAGCACCAGCAAGA---TAGCTGCCGCAAGCAGCTTAAGGGGGGTGAACCTCACGCCCTG 155
                                                                          CGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGACCCGTA 186
                                                                                                                                                                                                                                          276 AAAAGACGAAGAAGAAGAAGAAGAAGGACAGATGCAGAAGTGCTGCACAGAAATGAGCGA 335
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             GGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAAACCTGAGGCCCTG 126
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                                                                                             GTTTGAGAACAACCAAAGGTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAG
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                                                                                                                                           CAGC-----CCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGG-----
                                                                                                                                                                                                           ------CGCTGGATCCTCTCAGCACCAAGAGGTGTTGCAATGAGCTGAACGA
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: BM PC compatible

SECTION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAPLICATION DATE:

FILING DATE:

FLING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STAATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: de Lumen, Benito O.
APPLICANT: Galvez, Alfredo F.
TITLE OF INVENTION: Lunasin Peptides
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08938675A; Parent No. 6107287; GENERAL INFORMATION:
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US-08-938-675A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 GCT---GAGAAGCCCCAAATGCCAGTGCAAAGCGCTGCAGAAGATAATGGAGAACCAGAG 381
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 770
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.8%; Score 63.4; DB 3;
Best Local Similarity 51.6%; Pred. No. 2.7e-07;
Matches 369; Conservative 0; Mismatches 301;
REFERENCE/DOCKET NUMBER: B98-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                            LENGTH: 770 base pairs
TYPE: nucleic acid
STRANDEDINESS: double
TOPOLLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                      US-08-938-675A-1
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US-09-531-727-1
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y Sequence 8, Application US/09715036
y Sequence 8, Application US/09715036
y Patent No. 6943010
gENERAL INFORMATION:
APPLICANT: DODO, HOFFENSE W.
APPLICANT: DODO, HOFFENSE W.
APPLICANT: ARNTZEN, CHARLES J.
APPLICANT: VIQUEZ, OLGA
TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
TITLE OF INVENTION: DOMN-REQULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: DOMN-REQULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: DOMN-REQULATION NUMBER: US/09/715,036
CURRENT APPLICATION NUMBER: 60167,255
PRIOR APPLICATION NUMBER: 60167,255
NUMBER OF SEQ ID NOS: 8
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG 360
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439 TACTATGTGCAGGTTTGGACCCATGATCCAGTGCGACTTGTCCTCCGATGACTAAGAAGT 498
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                                           611 Greaargergarceraceraceraceraceragegeargegagegergregergreer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 62;
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; Fatent No. 5670367
; GENERAL INFORMATION:
    APPLICANT: SCHEIFLINGER, F.
    APPLICANT: SCHEIFLINGER, F.
    TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
    TUMBER OF SEQUENCES: 52
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Foley & Lardner
    STREET: 1800 Diagonal Road, Suite 500
    CITY: Alexandria
    STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Le
2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.6%; Score 62; DB 100.0%; Pred. No. 2.1 ative 0; Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 62; Conservative
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US-08-232-463-14/c
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US-09-715-036-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 AAAAGACGAAGAAGAAGAAGAAGAAGACACATGCAGAAGTGCTGCACAGAAATGAGCGA 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 CATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCTGCCCACGCATCTGCGAGGCAGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcagcaccagcaaga----ragcrigccgcaagcagcriccagggggggaaccrcacgcccrg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ceaeaagcacarcereeaeaagarccaaegccececeargaceargargargargacea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGC-----CCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63.4; DB 3; Length 77 Pred. No. 2.7e-07; 0; Mismatches 301; Indels
                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                  ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/531,727
FILING DATE: 21-MAR-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B98-003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      TITLE OF INVENTION: Lunasin Peptides
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/938,675
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-531-727-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 770 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    Alfredo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 8.8%;
Local Similarity 51.6%;
Hes 369; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                              ZIP: 94010
COMPUTER READABLE FORM:
                                                                                                                                                       STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 GCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGGATCCTCTC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 AGCACCAAGAGGGGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAGGTGCATGT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 GCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAGGCAACAGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 AGCAACAGTICAAGAGGGAGCTCAGGAACTIGCCTCAACAGIGCGGCCTTAGGGCACCAC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 AGCGTTGCGACTTGGACGTCGAAAGTGGCGGCAGAGACAGATACTAAACACTATCTCAA 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.2%; Score 58.8; DB 2; Length 7. Best Local Similarity 2.3%; Pred. No. 1.3e-05; Matches 9; Conservative 229; Mismatches 146; Indels
                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                 30472/114 IMMU
                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 7218 During TVPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                        FILING DATE
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US-08-618-911-1
; Sequence 1, Application US/08618911
; Patent No. 5850016
; PATENT INFORMATION:
APPLICANT: Jung, Rudolf

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Sequence 777, Application US/09949002

Patent No. 6900016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: MITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

FILE REFERENCE: CL000790

CURRENT APPLICATION NUMBER: US/09/949,002

CURRENT FILING DATE: 2000-01-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 ---CAGATGGAGAGAGAGCTCATGAACTTGGCTATTAGGTGCAGGTTGGGACCCATGATA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 CACATGCAGAAGTGCTGCAGCGAAATGAGCGAGCT----GAAAAGCCCCATATGCCAGTGC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 GAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAGGCAACAGGAG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 AAAGCGCTACAGAAGATAATGGATAACCAGAGCGAGCAACTGGAGGGGAAGGAGAAGAAG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 CAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAGGGCACCACAG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.6%; Score 54.4; DB 2; Length 723; Best Local Similarity 61.5%; Pred. No. 7.5e-05; Matches 123; Conservative 0; Mismatches 71; Indels
                                                      ALTERATION OF AMINO ACID COMPOSITIONS SEEDS
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,911
FILING DATE: Concurrently herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC
STREET: 700 Capital Square, 400 Locust Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Simon, Soma
REGISTRATION NUMBER: 37,444
REFERENCE/DOCKET NUMBER: 365-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       431 CGTTGCGACTTGGACGTCGA 450
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APPLICANT: Hastings, Craig
APPLICANT: Coughlan, Sean
APPLICANT: Hu, David
TITLE OF INVENTION: ALTERATIC
TITLE OF INVENTION: SEEDS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (515) 248-4844 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 723 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                ZIP: 50309
COMPUTER READABLE FORM:
                                                                                                                                                                                                         STREET: You TITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10..474
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LOCATION:
US-08-618-911-1
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488 AAAAAAGAAAAGAAAAGAAAAGAAATAGCTTATATATAAAGCTATTATCTATGGTTATGT 547
                                                                                                                                                                                                                                                                                                                                                                                                                       548 TTAGTTTTGGTAATAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTAACTAAGG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    608 CAAGCTTAGGTTATATGAGCACCTTTAGAGTGCTTTTATGGCGTTGTCTATGTTTTTGTTG 667
                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                   Query Match 6.8%; Score 48.4; DB 3; Length 25590; Best Local Similarity 50.9%; Pred. No. 0.016; Matches 115; Conservative 0; Mismatches 111; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     668 CTGCAGAGTTGTAACCATCTTGAAATATATAAAAAGATCATGTTT 713
PRIOR APPLICATION NUMBER: 60/231,401
NUMBER OF SEQ 1D NOS: 10823
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ 1D NO 777
LENGTH: 25590
TYPE: DNA
TYPE: DNA
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ 1D NO 777
LENGTH: 25590
TYPE: DNA
SOFTWARE: NAMEN: (10.77)
CARANISM: Mimman
SOFTWARE: NAMEN: (10.77)
CHER INPORMATION: (10.77)
US-09-949-002-777
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1: FEMC_Celerra_SIDS33/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
3: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
4: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
5: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
6: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
7: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
8: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
10: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
11: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
11: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
11: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
12: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
13: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
14: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
15: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
16: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
16: FEMC_Celerra_SIDS3/ptodata/2/pubpna/USIIA_PUBCOMB.seq:*
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Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 41, Appli
Sequence 41, Appli
Sequence 41, Appli
Sequence 121530,
Sequence 420, Appli
Sequence 6, Appli
Sequence 6, Appli
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                                                                                                      June 23, 2006, 18:12:55 ; Search time 980.107 Seconds
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GenCore version 5.1.9
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26 48.2 6.7 7758 7 28 47.8 48.2 6.7 758 7 29 47.8 6.7 1237 7 7 29 47.8 6.7 1237 7 7 46.2 6.6 1325 5 46.2 6.4 1325 5 46.2 6.4 1325 5 46.2 6.4 1325 5 46.2 6.4 1325 5 46.2 6.4 1325 5 46.2 6.4 1325 5 46.2 6.4 1325 5 46.2 6.4 1325 5 46.2 6.4 1325 5 47.4 66.2 6.4 1325 5 47.4 66.2 6.4 1069 10.4 45.5 6.4 6.8 6.8 6.4 6.8 6.8 6.8 6.8 6.8 6.8 6.8 6.8 6.8 6.8	.9-13 S
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30 47.6 6.6 451 8 32 46.4 6.5 325 11 33 46.4 6.5 945 11 34 46.2 6.4 1325 5 36 46.2 6.4 1325 5 37 46.2 6.4 1325 11 38 46 6.4 686 5 40 46 6.4 686 5 41 45.2 6.4 1069 11 44 45.2 6.3 5823 7 45.2 6.3 611 4	12-122633
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32 46.4 6.5 945 11 34 46.2 6.4 1325 14 35 46.2 6.4 1325 5 36 46.2 6.4 1325 5 37 46.2 6.4 1325 5 46 6.4 1325 5 46 6.4 1325 1 46 6.4 1325 1 46 6.4 1325 1 46 6.4 1325 1 47 46 6.4 686 5 41 46 6.4 1069 1 42 45.6 6.4 6063 7 43 45.2 6.3 611 4 45 2 6.3 611 4	19-76496
33 46.4 6.5 945 11; 35 46.2 6.4 1325 5 4 36 46.2 6.4 1325 5 1; 37 46.2 6.4 1325 1; 38 46 6.4 686 5 4 40 46 6.4 686 5 4 41 46 6.4 606 5 1 42 45.6 6.4 6063 7 43 45.2 6.3 611 4 45.2 6.3 611 4	80-585566
34 46.2 6.4 1325 4 36 46.2 6.4 1325 13 37 46.2 6.4 1325 15 38 46 6.4 1325 15 39 46 6.4 686 5 40 46 6.4 1069 11 41 45.6 6.4 6069 14 43 45.2 6.3 5823 7 45 45.2 6.3 611 4	JS-10-301-480-1198975 Sequence
35 46.2 6.4 1325 5 36 46.2 6.4 1325 11 38 46 6.4 686 4 39 46 6.4 686 5 41 46 6.4 1069 11 42 45.6 6.4 6063 7 43 45.2 6.3 5823 7 44 45.2 6.3 611 4 45 45.2 6.3 611 4	5A-19652 S
36 46.2 6.4 1325 11. 38 46.2 6.4 1325 11. 39 46 6.4 686 5 40. 40 46 6.4 1069 11. 41 46 6.4 1069 11. 42 45.6 6.4 1063 71. 43 45.4 6.3 5923 74. 44 45.2 6.3 611 44.	S-09-925-065A-19652 Sequence
37 46.2 6.4 1325 11. 38 46 6.4 686 5 40 46 6.4 1069 11. 41 46 6.4 1069 11. 42 45.6 6.4 1069 11. 43 45.4 6.3 5823 7 44 45.2 6.3 611 4 45.2 6.3 611 5	JS-10-301-480-120889 Sequence
38 46 6.4 686 4 39 46 6.4 686 5 41 46 6.4 1069 11 42 45.6 6.4 6063 7 43 45.2 6.3 611 4 45 45.2 6.3 611 4	JS-10-301-480-734298 Sequen
39 46 6.4 686 5 40 46 6.4 1069 11 42 45.6 6.4 1063 7 43 45.4 6.3 5823 7 44 45.2 6.3 611 5 45 45.2 6.3 611 4	S-09-925-065A-940622 Sequence 9
40 46 6.4 1069 11 42 45.6 6.4 1069 11 43 45.4 6.3 5823 7 44 45.2 6.3 611 4 45 45.2 6.3 611 5	S-09-925-065A-940622 Sequence
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42 45.6 6.4 6063 7 43 45.4 6.3 5823 7 44 45.2 6.3 611 4 45 45.2 6.3 611 5	JS-10-956-157-5342 Sequence
43 45.4 6.3 5823 7 44 45.2 6.3 611 4 45 45.2 6.3 611 5	S-10-240-453-267 Sequence
4 45.2 6.3 611 4 5 45.2 6.3 611 5	5-10-240-453-256 Sequence
5 45.2 6.3 6.11 5	S-09-925-065A-500442 Sequence
ALIGNMENTS	S-09-925-065A-500442 Sequence
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1 # 111000	

61 GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCCAGCTCGAGAGGCGAACCTGAG 120 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCCTCGCCGCGCCCACCGCATCTGCGAGGCA 61 GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAG 121 GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTGG 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTTCCTCCTCGCTGCCCACGCATCTGCGAGGCA 121 GCCCTGCGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTGG Gaps °, Match 100.0%; Score 717; DB 3; Length 717; Local Similarity 100.0%; Pred. No. 5.4e-177; les 717; Conservative 0; Mismatches 0; Indels Sequence 2, Application US/09731375A
Publication No. US20030035810A1
GENERAL INFORMATION:
APPLICANT: Caplan, Michael
TITLE OF INVENTION: Michael
FILE REPERENCE: 2002834-0100
CURRENT APPLICATION NUMBER: US/09/731,375A
CURRENT FILING DATE: 2002-11-13
PRIOR PAPLICATION NUMBER: 60/195,035
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 717 ORGANISM: Arachis hypogaea US-09-731-375A-2 US-09-731-375A-2 TYPE: DNA 181 Query Match Best Loca Matches 엄 ò 임 ò g ઠ ò

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100.0%; Pred. No. 5.4e-177;
iive 0; Mismatches 0;
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Sequence 2, Application US/10728051
Fublication No. US20040234548A1
GENERAL INFORMATION:
APPLICANT: Caplan, Michael J.
APPLICANT: Socin B., Howard
APPLICANT: Sampson A., Hugh
TITLE OF INVENTION: Microbial Delivery System
FILE REFERENCE: 2002834-022
CURRENT APPLICATION NUMBER: US/10/728,051
CURRENT FILING DATE: 2003-12-04
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2000-12-05
PRIOR FILING DATE: 2000-12-05
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 717
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ORGANISM: Arachis hypogaea
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Best Local Similarity 100.
Matches 717; Conservative
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                        ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAG 300
                                                                                   GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG 360
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    ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gollan, Michael J.
APPLICANT: Bottomly H., Kim
APPLICANT: Sosin B., Howard
APPLICANT: Bottomly H., Kim
APPLICANT: Bottomly H., Kim
APPLICANT: Burks A., Wesley
APPLICANT: Sampson A., Hugh
ITLE OF INVENTION: Microbial Delivery System
FILE REFERENCE: 2002834 0232
CURRENT APPLICATION NUMBER: US/10/728,323
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: 60/195,035
PRIOR APPLICATION NUMBER: 09/731,375
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 3
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO 2.
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CRGANISM: Arachis hypogaea
US-10-728-323-2
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Best Local Similarity 100.
Matches 717; Conservative
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US-10-228-806-3

US-10-228-906-3

Sequence 3, Application US/10228806

Publication No. US20030049237A1

GENERAL INFORMATION:

APPLICANT: Bannon. et al.

TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions

TITLE OF INVENTION: Lo Allergy

FILE REFRENCE: 2002834-0043

CURRENT APPLICATION NUMBER: US/10/228,806

NUMBER OF SEQ ID NOS: 81

SEQ ID NOS: 81

SEQ ID NOS: 81

SEQ ID NOS: 81
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1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCGCTGCCCACGCATCTGCGAGGCA
                                   GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGGGCTCGAGAGGGGCGAACCTGAG
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Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 474; Conservative 0; Mismatches 0;
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Publication No. US200500639941

GRNERAL INFORMATION:
APPLICANT: Caplan, Michael J.
APPLICANT: Sampson, Hugh A.
APPLICANT: Burks, A. Wesley
APPLICANT: Bottomly, Kim H.
APPLICANT: Bottomly, Kim H.
APPLICANT: Bottomly, Kim H.
TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction to Allergy
FILE REFERENCE: 2002834-0233
CURRENT APPLICATION NUMBER: US/10/899,551
CURRENT FILING DATE: 2004-07-26
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.2
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US-10-899-551-3
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Best Local Similarity 100.
Matches 717; Conservative
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US-10-899-551-3
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APPLICANT: DODO, HORTENSE W.
APPLICANT: ARNTZEN, CHARLES J.
APPLICANT: KONAN, KOFFI N'DA
APPLICANT: VIQUEZ, OLGA
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
FILE REPRENCE: 072121/0104
CURRENT APPLICATION NUMBER: US/10/958,324
CURRENT FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 60/011-20
PRIOR FILING DATE: 099-11-19
NUMBER OF SEQ ID NOS: 8
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                    301 TGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGGGATAGGTTGCAGGGGAGG
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TGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAGG
                                                                             362 CAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGCGGCCTTAGG
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                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/10958324; Publication No. US20050114924A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 682
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US-10-958-324-3
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US-100-3034-62
US-10-100-3034-62
; Sequence 62. Application US/10100303A
; Publication No. US2003202980A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction
; TITLE OF INVENTION: A Allargy
; FILE REFERENCE: 2002834-0166
; CURRENT APPLICATION NUMBER: US/10/100,303A
; NUMBER OF SEQ ID NOS: 138
; NUMBER OF SEQ ID NOS: 138
; SOFFWARE: Patentin Ver. 2.1
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                    CAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAGG
                                          61 CAGTGGGAACTCCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGGGGAACCTGAGG
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P. ORGANISH Arachis hypogaea, Prot/Nucleo Ara h 2
US-10-100-303A-62
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TYPE: DNA
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                                                                                                                                     FULLICALUL INFORMATION:

APPLICANT: DODO, HORTENSE W.
APPLICANT: DODO, HORTENSE W.
APPLICANT: ARNIZEN, CHARLES J.
APPLICANT: TONAN, KOFFI N'DA
APPLICANT: TONAN, KOFFI N'DA
TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
TITLE OF INVENTION NUMBER: US/10/958,324
CURRENT FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: 60/167,255
PRIOR FILING DATE: 1999-11-19
SPRIOR FILING DATE: 1999-11-19
SOFTWARE: PATENTING DATE: 2010-11-19
SOFTWARE: PATENTING DATE: 2010-11-19
SOFTWARE: PATENTING DATE: 2010-11-19
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487 GCCACCACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCAG 528
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Best Local Similarity 100.0%; Pred. No. 4.3e-110;
Matches 462; Conservative 0; Mismatches 0;
                                                                                                      ; Sequence 1, Application US/10958324
; Publication No. US20050114924A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Arachis hypogaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (110)..(730)
US-10-958-324-1
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US-10-958-324-7
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which was the same

; Sequence 7, Application US/10958324 ; Publication No. US20050114924A1

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APPLICANT: EAROSE Thomas J
APPLICANT: Kovalic David K
APPLICANT: Even Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 26383
LENGTH: 1013
APPLICANT: DODO, HORTENSE W.

APPLICANT: ARNTZEN, CHARLES J.

APPLICANT: KORAN, KOFFI N'DA

APPLICANT: VIQUEZ, OLGA

TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN

TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS

FILE REFERENCE: 072121/0104

CURRENT FALLING DATE: 2004-10-06

PRIOR FILING DATE: 2004-11-20

PRIOR FILING DATE: 1999-11-19

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

LENGTH: 80

TYPE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.2%; Score 80; DB 10; L
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 80; Conservative 0; Mismatches 0;
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LOCATION: (1)..(1013)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                            8.8%; Score 63.4; DB 7;
.larity 51.6%; Pred. No. 9e-06;
Conservative 0; Mismatches 301;
PILING DATE: <Unknown>
ATTOREZ/AGENT INPORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 898-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
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H
                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                           TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                TYPE: CDNA
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es 369; Conserv
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US-10-958-324-8
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  CGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGACCCGTA 186
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                                                                                                          193 CGAGAAGCACATCATGGAGAAGATCCAAGGCCGCGGCGATGACGATGATGATGATGACGA
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COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-No. US20030229038A1-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/531,727
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STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
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INVENTION: Lunasin Peptides
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APPLICATION NUMBER: 08/938,675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/302,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10302633
Publication No. USZ00330229038A1
GENERAL INFORMATION:
APPLICANT: de Lumen, Benito O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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US-10-302-633-1
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402 438 498 521 555

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127 CGAGCAACATCTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGACCCGTA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                           403 TCAACAGTGCGGCCTTAGGGCACCACAGCGTTGCGACTTGGACGTCGA
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US-10-424-599-121530
; Sequence 121530, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 GGGTGCGACTTGTCCTCCGA 461
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; OTHER INFORMATION: 2S albumins 1
US-10-508-263-41
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                                                      APPLICANT: DODO, HORTENSE W.
APPLICANT: DODO, HORTENSE W.
APPLICANT: DODO, HORTEN, CHARLES J.
APPLICANT: KONAN, KOFFI N'DA
APPLICANT: WONAN, KOFFI N'DA
TITLE OF INVENTION: DOMN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
FILE REFERENCE: 07212/0104
CURRENT APPLICATION NUMBER: US/10/958,324
CURRENT FILING DATE: 2004-110-06
PRIOR APPLICATION NUMBER: US/09/715,036
PRIOR PLING DATE: 2000-11-20
PRIOR PLING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NOS: 8
SOFTWARE: PATENTIN VEY: 2.1
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Sequence 43, Application US/10508263
Sequence 43, Application US/10508263
Publication No. US20050260754A1
GENERAL INFORMATION:
APPLICANT: BASF Plant Science GmbH
TITLE OF INVENTION: Constructs and methods for regulating gene expression
FILE SFERENCE: 5326-20085.00
CURRENT APPLICATION NUMBER: US/10/508,263
CURRENT FILING DATE: 2004-09-20
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAGAGCGATAGGTTGCAGGGGAG
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8.3%; Score 59.2; DB 10; Length 477;
Best Local Similarity 53.8%; Pred. No. 9e-05;
Matches 252; Conservative 0; Mismatches 183; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Probe US-10-958-324-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.6%; Score 62; DB 10; Length 62; Best Local Similarity 100.0%; Pred. No. 6e-06; Matches 62; Conservative 0; Mismatches 0; Indels
Sequence 8, Application US/10958324
Publication No. US20050114924A1
GENERAL INFORMATION:
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; OTHER INFORMATION: 2S albumins
US-10-508-263-43
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ORGANISM: Artificial Sequence
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129 CGAGAAGCACATCATGGAGAAGATCCAAGGCCGCGGGCGATGACGATGATGATGATGATGATGA
                                                                                                                                              189 CGACAATCACATTCTCAGGACCATGCGGGAAGAATCAACTACATAAGGAGGAACGAAGG 248
                                                                                                                                                                                                                             ---AGGCGCTGGATCCTCTCAGCACCAAGAGGTGTTGCAATGAGCTGAACGA 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 CGAGGAACTGGAGGAGAAGAAGAAGAAGAA---ATGGAGAAGGAGCTCATTAACTTGGC 422
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                                                                                                                                                                                                                                                                                                        249 AAAAGACGAAGACGAAGAAGAAGAAGAAGACACATGCAGAAGTGCTGCACAGAAATGAGCGA 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-508-263-41
Sequence 41, Application US/10508263
Sequence 41, Application US/10508263
Publication No. US20050260754A1
GENERAL INFORMATION:
TITLE OF INVENTION: Constructs and methods for regulating gene expression
FILE REFRENCE: 53262-20085.00
CURRENT APPLICATION NUMBER: US/10/508,263
CURRENT APPLICATION NUMBER: 2004-09-20
NUMBER OF SEQ ID NOS: 126
SOCTHARE: PALENTIN Ver. 2.1
SEQ ID NO 41
LENGTH: 468
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                                                                       187 CAGC-----CCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAG-----
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 121530
LENGTH: 883
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_80749C.1
US-10-424-599-121530
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Search completed: June 24, 2006, 01:56:18 Job time: 981.107 secs

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ORGANISM: Glycine max US-10-953-349-13196
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Best Local Similarity
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/EMC_Celerra_SIDS3/ptcdata/1/pubpna/USO6_NEW_PUB.seq:*
/EMC_Celerra_SIDS3/ptcdata/1/pubpna/USO7_NEW_PUB.seq:*
/EMC_Celerra_SIDS3/ptcdata/1/pubpna/USO8_NEW_PUB.seq:*
/EMC_Celerra_SIDS3/ptcdata/1/pubpna/USO8_NEW_PUB.seq:*
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/EMC_Celerra_SIDS3/ptcdata/1/pubpna/USIO_NEW_PUB.seq:*
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                                                                                                           June 23, 2006, 18:21:18 ; Search time 15.6052 Seconds
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               GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-517-441-443
US-10-517-441-443
US-10-517-441-443
US-10-517-441-443
US-10-517-441-597
US-10-517-441-593
US-10-517-441-730
US-10-517-441-423
US-10-517-441-423
US-10-517-441-423
US-10-517-441-423
US-10-517-441-499
US-10-517-441-499
US-10-517-441-499
US-10-517-441-499
US-10-517-441-773
US-10-517-441-499
US-10-517-441-773
US-10-517-441-697
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US-10-517-441-697
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Maximum Match 100%
Listing first 45 summaries
                                                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Maximum DB
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Sequence 13196, Application US/10953349
Sequence 13196, Application US/10953349
Sequence 13196, Application US/20060107345A1
GENERAL INFORMATION
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 13196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 CACCAAGAGGGGTGTTGCAATGAGCTGAACGAGTTTGAGAACAACCAAAGGTGCATGTGC
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US-10-449-902-27048
US-10-517-441-293
US-10-517-441-293
US-10-517-441-567
US-10-517-441-318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54.4; DB 6;
Pred. No. 3.5e-05;
0; Mismatches 71;
                                                                                                                                                                                                                                                     US-10-517-441-714
US-10-517-441-308
US-10-517-441-582
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Publication No. US20060121467A1
GENERAL INFORMATION:
APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTGCGACTTGTCCTCCGA 487
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261789
6432
9859
16843
9859
9850
8802
8802
8802
8602
6175
8603
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APPLICANT: NeuroNova AG
TITLE OF INVENTION: A Method for Diagnosing and Treating Affective Disorders
FILE REFERENCE: XXX
CURRENT APPLICATION NUMBER: US/10/553,298
CURRENT FILING DATE: 2005-10-14
NUMBER OF SEQ ID NOS: 111
SOFTHARE: PatentIn version 3.1
LENGTH: 56580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-517-441-443
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
6.0%; Score 43; DB 6; Length 8172;
Best Local Similarity 55.8%; Pred. No. 0.1;
Matches 82; Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6825 racraaarraarraraaarrakeer 6799
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR PILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 443
LENGTH: 8172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587 TGTTGATCGTGTTAACTAAGGCAAGCT 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10553298 Publication No. US20060110385A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: exon6
LOCATION: (35416)..(35496)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (32481)..(32577)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24841) . . (25009)
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NAME/KEY: exon1
LOCATION: (3000)..(3124)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon3
LOCATION: (26134).
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (24841).
OTHER INFORMATION:
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LOCATION: (3095)
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LOCATION: (3248:
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                                                                                                     APPLICANT: NULLAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: COME, Maxime P.
APPLICANT: HOBFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
TITLE OF INVENTION: Motor 12004-12-11
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: DC1/EP2003/010881
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2001-07
PRIOR FILING DATE: 2001-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2001-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.0%; Score 43.2; DB 6; Length 8172; Best Local Similarity 52.8%; Pred. No. 0.089; Matches 93; Conservative 0; Mismatches 83; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferative disorders
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APPLICANT: MARX, Almuch
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-10-517-441-443/c
Sequence 443, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
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APPLICANT: FORKENS, John
APPLICANT: FORKENS, John
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, INKO
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Marmin
APPLICANT: SCHMITT, Marmin
APPLICANT: LOOK, Maxime P.
APPLICANT: MAXIME P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                  MARTENS, John
MODEL, Fabian
NIMMRICH, Inko
RUJAN, Tamas
                                     APPLICANT:
APPLICANT:
                                                                                               APPLICANT
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126 TTTTGGTATTCATAAATTTTATGCCGGCAAGAATATG 162
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Publication No. US20060115490A1

GENERAL INFORMATION:
APPLICANT: CHIRON SpA

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REPERENCE: P026927W0
CURRENT APPLICANT: 003.09-12
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT AILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 969
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 AAAAGAAAAGAAAATAGCTTATATATAAGCTATTATCTATGGTTATGTTTAGTTTTG 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.8%; Score 41.8; DE Best Local Similarity 59.8%; Pred. No. 0.5; Matches 70; Conservative 0; Mismatches
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; ORGANISM: Staphylococcus aureus
US-10-471-571A-969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | NAME/KEY: exon13
| LOCATION: (54392)...(54889)
| OTHER INFORMATION:
| US-10-553-298-1
                   NAME/KEY: exon7
LOCATION: (36113)..(36242)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: exon11
LOCATION: (47380)..(47529)
OTHER INFORMATION:
                                                                               FEATURE:
NAME/KEY: exon8
LOCATION: (37541)..(37677)
OTHER INFORMATION:
                                                                                                                                                              FEATURE:
NAME/KEY: exon9
LOCATION: (45470)..(45560)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                     NAME/KEY: exon10
LOCATION: (47229)..(47295)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (50438)..(50539)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: exon12
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US-10-471-571A-969
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APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
PRIOR APPLICATION NUMBER: DC4-12-11
PRIOR APPLICATION NUMBER: DC7/EP2003/010881
PRIOR APPLICATION NUMBER: DE 1031055.0
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-61-17
PRIOR FILING DATE: 2003-61-17
PRIOR PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-01
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WS-11-217-529-166179/C

Sequence 166179, Application US/11217529

Publication No. US20060099612A1

GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAN, YOSHIHIRO
APPLICANT: RODAMA, YUKIKO
APPLICANT: RODAMA, YUKIKO
APPLICANT: RUNIMIRA, TOMOKO
APPLICANT: RUNIMIRA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, 109111X0
FILE REFERENCE: S-38-285
CURRENT FILINO NUMBER: US/11/217,529
CURRENT FILINO DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
SEQ ID NO 166179
SEQ ID NO 166179
AUDE: NUMBER OF SEQ ID NOS: 197023
SEQ ID NO 166179
AUDE: NUMBER OF SEQ ID NOS: 197023
AUDE: NUMBER OF SEQ ID NOS: 197024
AUDE: NUMBE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: WAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, INKO
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: MARK, Almuth
APPLICANT: MARK, Almuth
APPLICANT: MARK, Almuth
APPLICANT: MARK, Heinz
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TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell, ITLE OF INVENTION: proliferative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.5%; Score 39.4; DB 6; Length 6521; Best Local Similarity 59.3%; Pred. No. 0.78; Matches 67; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: proliferative disorders rich Reference 47675-93 CURRENT APPLICATION NUMBER: US/10/517,441 CURRENT APPLICATION NUMBER: US/10/517,441 CURRENT FILING DATE: 2004-12-11 PRIOR APPLICATION NUMBER: PCT/EP2003/010881 PRIOR FILING DATE: 2003-10-01 PRIOR APPLICATION NUMBER: DE 10310096.8 PRIOR FILING DATE: 2003-04-17 PRIOR PLING DATE: 2003-01-07 PRIOR PLING DATE: 2003-01-07 PRIOR FILING DATE: 2002-10-01 NUMBER OF SEQ ID NOS: 2147
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10S-10-217-441-730/C

5 Sequence 730, Application US/10517441

5 Publication No. US20060121467A1

GENERAL INFORMATION:

APPLICANT: POEKENS, John

5 APPLICANT: MARBECK, Nadia

5 APPLICANT: MAIER, Sabine

5 APPLICANT: MAREN, John

6 APPLICANT: MODEL, Fabian
                                                                                                                                                                                                                                                                                                  Sequence 583, Application US/10517441
Publication No. US20060121467A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FOEKENS, John
APPLICANT: HARBEK, Nadia
APPLICANT: KORNIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MORDEL, Fabian
APPLICANT: NIMMRICH, Inko
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SCHMITT, Manfred
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MARX, Almuth
HOEFLER, Heinz
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                                                                                                                                                                                                                                                                           US-10-517-441-583
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APPLICANT:
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APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
APPLICANT: LOOK, Maxime P.
APPLICANT: HARFINE APEN
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: PRION EL 2003-10-33
CURRENT APPLICATION NUMBER: DE 103/10/811
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
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                                                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-517-441-697
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                                                                                                                                                                                                                  Query Match 5.6%; Score 40.2; DB 6; Length 4857; Best Local Similarity 48.1%; Pred. No. 0.42; Matches 114; Conservative 0; Mismatches 123; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 309, Application US/10517441
Publication No. US20060121467A1
GENERAL INFORMATION:
APPLICANT: FOEKENS, John
APPLICANT: KOEKIG, Thomas
APPLICANT: MARBECK, Nadia
APPLICANT: MARREK, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, INKO
APPLICANT: RUJAN, Tamas
                                                        TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                  LENGTH: 4857
SEQ ID NO 697
                                                                                                                 FEATURE:
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APPLICANT: HOBFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
FULE REFERENCE: 47675-93
CURRENT APPLICATION WUMBER: US/10/517,441
PRIOR APPLICATION UNMBER: PCT/BP2003/010881
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                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                               Length 8900;
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                                                                                                                                                                                                                                                                                                                                                  52; Indels
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                                                                                                                                                                                                                                                                                               Score 38.8; DB 6;
Pred. No. 1.3;
0; Mismatches 52;
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PRIOR APPLICATION NUMBER: DE 10300096.8 PRIOR FLILNG DAFE: 2003-01-07 PRIOR PRIOR APPLICATION NUMBER: DE 10245779.4 PRIOR FILING DATE: 2002-10-01 SEQ ID NOS: 2147 SEQ ID NO 428 LENGTH: 8900
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PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779-4
PRIOR FILING DATE: 2002-10-07
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                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.4%;
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No. US20060121467A1 GENERAL INFORMATION:
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SCHMITT, Armin
SCHMITT, Manfred
LOOK, Maxime P.
MARX, Almuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MATER, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, Inko
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SEQ ID NO 702
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                     APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: MARX, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
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ilarity 54.5%; Pred. No. 1.2;
Conservative 0; Mismatches 65; Indels
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/517,441

CURRENT FILING DATE: 2004-12-11

PRIOR APPLICATION NUMBER: PCT/EP2003/010881

PRIOR FILING DATE: 2003-10-01

PRIOR APPLICATION NUMBER: DE 10317955.0

PRIOR FILING DATE: 2003-04-17

PRIOR FILING DATE: 2003-04-17

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2003-01-07

PRIOR FILING DATE: 2003-01-01
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APPLICATION NUMBER: PCT/EP2003/010881
FILING DATE: 2003-10-01
APPLICATION NUMBER: DE 10317955.0
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CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/BE2003/01086
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Publication No. US20060121467A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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SCHMITT, Armin
SCHMITT, Manfred
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HARBECK, Nadia
KOENIG, Thomas
MAIER, Sabine
MARTENS, John
MODEL, Fabian
NIMMRICH, Inko
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NIMMRICH, Inko
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SEQ ID NO 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell TITLE OF INVENTION: proliferative disorders FILE REPERORCE: 4767-9781.

CURRENT APPLICATION NUMBER: US/10/517,441

CURRENT FILING DATE: 2004-12-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 15355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURKENT FILING DATE: 2004-12-11

PRIOR PELICATION NUMBER: PCT/EP2003/010881

PRIOR FILING DATE: 2003-10-01

PRIOR PELING DATE: 2003-04-17

PRIOR PILING DATE: 2003-04-17

PRIOR PILING DATE: 2003-01-07

PRIOR PILING DATE: 2003-01-07

PRIOR PILING DATE: 2003-01-07

PRIOR PILING DATE: 2003-01-07

PRIOR PILING DATE: 2002-10-01

NUMBER OF SEQ ID NOS: 2147

LENGTH: 15355
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US-10-517-441-689
US-10-517-441-689
; Sequence 689, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INPORMATION:
; APPLICANT: HARBECK, Nadia
; APPLICANT: HARBECK, Nadia
; APPLICANT: MARIEK, Sabine
; APPLICANT: MARIEK, Sabine
; APPLICANT: MARIEK, John
                                                               Sequence 415, Application US/10517441 Publication No. US20060121467A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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SCHMITT, Manfred
LOOK, Maxime P.
MARX, Almuth
                                                                                                                                       APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KORNIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, Inko
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APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manier
APPLICANT: SCHMITT, Manier
APPLICANT: SCHMITT, Manier
APPLICANT: SCHMITT, Manier
APPLICANT: MARX, Almuth
APPLICANT: MOSTON: Method and nucleic acids for the improved treatment of breast cel
TILE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TILE OF INVENTION: MOSTON MARER: US/10/517,441
CURRENT FILING DATE: 2003-10-01
PRIOR PLING DATE: 2003-10-01
PRIOR PLING DATE: 2003-10-01
PRIOR PLING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2003-10-07
PRIOR SEQ ID NOS: 2147
                                                                                                                                            521 TATATAAGCTATTATCTATGGTTATGTTTTGGTAATAATAAAGATCATCACTATA 580
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Pred. No. 1.1;
0; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                            Sequence 423, Application US/10517441 Publication No. US20060121467A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.4%;
Best Local Similarity 47.7%;
Matches 113; Conservative (
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ORGANISM: Artificial Sequence
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MARTENS, John
MODEL, Fabian
NIMMRICH, Inko
RUJAN, Tamas
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APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
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US-10-517-441-423/c
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APPLICANT: NIMMERCH. INC.
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: HORFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
TITLE OF INVENTION: Morbins: US/10/517,441
TITLE OF INVENTION NUMBER: US/10/517,441
CURRENT APPLICATION NUMBER: US/10/517,441
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 689
TENERAL 15355
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-689
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ORGANISM: Artificial Sequence
MODEL, Fabian
NIMMRICH, Inko
RUJAN, Tamas
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Perfect score:

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Intrabalies sequences.

Sosin,H., Banon,G.A., Jr,W.A.B. and Sampthon,H.A.
Methods and reagents for decreasing allergic reactions
MulveRSITY OF MEW YORK, HOWARD SOSIN
UNIVERSITY OF NEW YORK, HOWARD SOSIN
OS Arachty OF NEW YORK, HOWARD SOSIN
DE 20-JAN-1998 US 60/073283,13-FEB-1998 US 60/074633 PR
OS OF 11-1280 US 60/074624,13-FEB-1998 US 60/074633 PR
OS OF 11-1280 US 09/074624,13-FEB-1998 US 09/074633 PR
OS OF 11-1280 US 09/074624,13-FEB-1998 US 09/074633 PR
OS OF 11-1280 US 09/074624,13-FEB-1998 US 09/074633 PR
OS OF 11-1280 US 09/074624,13-FEB-1998 US 09/074633 PR
OS OF 09/074624,13-FEB-1998 US 09/074624
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AR615282 Sequence
AX839958 Sequence
AX800494 Glycine m
BD175911 Regulatio
AR202576 Sequence
AR615280 Sequence
AX840475 Sequence
AX840475 Sequence
AX841313 Sequence
AX13319 Glycine max
E02463 CDMA encodi
AR625313 Sequence
AX25313 Sequence
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AX625313 Sequence
AX641066 Sequence
AX25313 Sequence
AX641066 Sequence
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AX641067 Sequence
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AX641047 Sequence
AX646464 Sequence
AX641047 Sequence
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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Pred. No. 0;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                AR202576
AR486463
AR615280
AX839950
AX840475
AB113349
E32414
AR341131
SOYGEVEBU
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AR202577
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AX840477
AB113350
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AB030494
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Score

Result No.

us-10-728-051-3.rge

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PAT 22-JUN-2001

(US) YORK

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Arachis hypogaea (peanut)
Arachis hypogaea
Arachis hypogaea
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae,
Aeschynomeneae, Arachis.
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    /organism="Arachis hypogaea"

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/protein_id="AAC63045.1"

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/t anslation="ROQPEENACCPCRLNAQRPDNRIESEGGYIETWNPNNGFFECAG

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VALSRLVLRRNALERPYSNAPOELFTQGROYFGLIFPGCPRHYEEPHTQGRRSQSO

VALSRLVLRRNALERPSHOKYHRFDEGDLIAVPTGVAFWLYNDHJTDVVAVSLTDTN

NNDNGLJOFPRRFNLAGNTEGDELRYQQGSRGSRRSLPSPSPSPGSQPRQERREFSP

RGQHSRRERAGQEEBENGGGNIFSGFTPEFLEQAFQVDDRQIVQNLGGSTFESEEGAIY

TVRGGLRILSPDRKRRADEEEEYDEDEYEYDEBERGGSRGGGSRGRGGIETTTCTASAK

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INTRLRGRAHVQVVDSKGNRYVDELGGGHYLVVPQNRSAKSGSBNFEYVAFKTDS

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Arachis hypogaea
Bukaryota; Viridiplante; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplante; Streptophyta; Embryophyta; Tracheophyta;
Bermarcphyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Asschynomenees, Arachis.
1 (bases 1 to 1902)
Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.Z.
Isolation of peanut genes encoding arachins and conglutins by
Plant Sci. 169 (2), 439-445 (2005)
2 (bases 1 to 1903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
3 (bases to 1902)
Yan, Y., Wang, L. and Huang, S.
Direct Submission
Submitted (03-DEC-2004) Department of Biology and Biotechnology,
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San,Y., Wang,L. and Huang,S.
CDNA clone of peanut seed storage protein
Unpublished
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1 (bases 1 to 1853)

Dodo,H.W., Arntzen,C.J., Viquez,O.Down-regulation and silencing of a peanut seeds
Patent: US 6943010-A 4 13-SEP-2005
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/mol_type="genomic DNA"
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                                                         / translation="MAKLLELSPCFCFLVLGASSISFRQQPEENACGFGRLNAQRPDN
RIESEGGYIETWNPNNQEFECAGVALSRLVLRRNALRRPFYSNAPQEIFIQGGRGYFG
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SAEKGGSRGGNGIEETCTASYKKNIGRNRSPDIYNPQAGSLKTANDLMLLILRWLGL
QNFAVAGKSQSDNFEYVAFKTDSRPSIANLAGENSVIDNLPEEVVANSYGLQREQARQ
QLKNNNPFKFFVPPSQQSPRAVA"
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                                                                                                                              TTGTTTGTCGCTCACTACAACACCCACCACCACCATCATATATCGATTGAGGGGACGG
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Down-regulation and silencing of allergen genes in transgenic
peanut seeds
Patent: WO 0136621-A 4 25-MAY-2001;
Alabama A & M University (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db zref="taxon:3818"
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91.3%; Score 1391.2;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches
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AX148741 GI:14347295
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           Length 1853;
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                                                    Indels
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           B
         Score 1391.2;
                            Pred. No. 0;
0; Mismatches
       Query Match
Best Local Similarity 95.4%;
Matches 1454; Conservative
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PLN 29-SEP-1999

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SKleber-Janke, T.

SKleber-Janke, T.

Direct Submission

AL Submitted (125-AUG-1998) Biochemische und Molekulare Allergologie,

Borschungszentrum Borstel, Parkallee 22, Borstel 23845, Germany

SC Location/Qualifiers

1. 1853

1. 1853

Arachis hypogaea"

//mganism="Nrachis hypogaea"

//mganism="Nrachis hypogaea"

//mb_type="nRNa"

//db_rref="nRNa"

//db
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GVAFWLYNDHDTDVANSLTDTNNNDNQLOQFPRRFNLAGNHEQBEFLRAPF
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RRGRGSRGGGNGIEETICTACVKKNIGGNRSPHIYDPQRWFTQNCHDLNLLILRWLGI
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Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Stosids; eurosida I.; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
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GCTCACGTGCAAGTCGTGGACAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAG
                                                                            GGTCACGTGCTTGTGGTGCCACACACTTCGCCGTCGCTGGAAAGTCCCAGAGCGAGAAC
                                                                                                 TTCGAATACGTGGCATTCAAGACAGACTCAAGGCCCAGCATAGCCAACCTCGCCGGTGAA
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Kleber-Janke,T., Crameri,R., Appenzeller,U., Schlaak,M. and
Becker,W.M.
Selective cloning of peanut allergens, including profilin and
albumins, by phage display technology
Int. Arch. Allergy Immunol. 119 (4), 265-274 (1999)
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AF086821 GI:5712198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="seed storage protein; allergen"
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                                                                                                                                                                                                                                                                                                                                                                                             1. .1593
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ACCESSION
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                                     AATGCGCCGGCGTCGCCTCTCTCGCTTAGTCCTCCGCCGCAACGCCCTTCGTAGGCCTT
                                                                                             TATTCCCTGGTTGTCCTAGCACATATGAAGAGCCTGCACAACAAGACGCCGATATCAGT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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Jain,A.K. and Basha,S.M.
Direct Submission
Submitted (22-AUG-2000) Plant Biotechnology, Florida A&M
University, 301 South Perry Paige Building, Tallahassee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jain A.K. and Basha S.M.
Direct Submission
Submitted (02-FEB-1999) Plant Biotechnology, Florida A&M
University, 301 South Perry Paige Building, Tallahassee,
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Molecular cloning of a glycinin-type peanut seed
Unpublished
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Arachis hypogaea Glyl (Glyl) mRNA, complete cds.
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On Aug 22, 2000 this sequence
Location/Qualifiers
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Arachis hypogaea
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae,
             TGCAAAACCTAAGAGGCGAGACCGAGAGTGAAGAGAGGGGAGCCATTGTGACAGTGAGGG
                                                                                                      GAGGCCTCAGAATCTTGAGCCCCAGATAGAAAGAGACGTGCCGACGAAGAAGAGGAATACG
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 ACAGATCCCCTGACATCTACAACCCTCAAGCTGGTTCACTCAAAACTGCCAACGATCTCA
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        /organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="Florunner"
                                                                                                                                                                                                                                                                                   Query Match 90.1%; Score 1373.2; Best Local Similarity 94.8%; Pred. No. 0; Matches 1446; Conservative 0; Mismatches
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/db_xref="Gl:9864777"
                                    /db_xref="taxon:3818"
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Yan,Y., Wang,L. and Huang,S.
Direct Submission
Submitted (30-JUL-2004) Department of Biology and Biotechnology,
Submitted (30-JUL-2004) GuangZhou, GuangDong 510275, China
Location/Qualifiers
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Aeschynomeneae; Arachis.
1 (bases 1 to 1901)
Yan Y.S., Lin, X.D., Zhang Y.S., Wang,L., Wu,
Isolation of peanut genes encoding arachins
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                                      expressed sequence tags
Plant Sci. 169 (2), 439-445 (2005)
2 (bases I to 1901)
2 Van, Y., Wang, L. and Huang, S.
CDNA clone of peanut seed storage protein Unpublished
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/organism="Arachis hypogaea"
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/db_xref="taxon:3818"
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Pred. No. 0;
0; Mismatches
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                                                    JOURNAL
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1 (bases I to 1934)

S Yan, Y. S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.Z.
Isolation of peanut genes encoding arachins and conglutins by expressed sequence tags

I Plant Sci. 169 (2), 439-445 (2005)

E 2 (bases I to 1934)

S Yan, Y., Wang, L. and Huang, S.
CDNA clone of peanut seed storage protein gene
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/product="arachin Ahy-1"
/product="arachin Ahy-1"
/product="arachin Ahy-1"
/product="arachin Ahy-1"
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PSYSYSPOTOPYQENERESPRGQEGGENEGGNIFSGFFRRSL
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PSYSYSPOTOPYQENERENAGGARENAGGARENAGNUD
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BRQHDRRRGRGSRGSGNGIEETICTASFKKNIGRNRSPDIYNPQAGSLKTANELNLLI
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HVLVVPQNFAVAGKSQSENFEYVAFKTDSRPSIANLAGENSFIDNLPEEVVANSYGLP
REQARQLKNNNPFKFFVPPSEQSLRAVA"
                                                   08-JUL-2005
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/organism="Arachis hypogaea"
/mol_type="mRNA"
/db_xref="taxon:3818"
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larity 92.8%; Pred. No. 0;
Conservative 0; Mismatches
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Yan, Y., Wang, L. and Huang, S.
Direct Submission
Submitted (30-JUL-2004) Department
Sun Yat-sen University, GuangZhou,
Location/Qualifiers
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Arachis hypogaea
                                                                  Arachis hypogaea arachir
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Qy 1355 CCAGCATAGCCAACCTCGCCGGTGAAAACTCCGTCATAGATAACCTGCCGGAGGAGGTGG 1414 Db 1500 CCAGCATAGCCAACCTAGCCGGTGAAAACTCCTTCATAGATAACTTGCCGGAGGAGGTGG 1559 Qy 1415 TTGCAAATTCATATGGCCTCCAAAGGAGGAGGCAGCTAAGAACAACCCCT 1474 Db 1560 TTGCAAATTCATATGGCCTCCCAAAGGAGGAGCAGCAAGCTTAAGAACAACCCCT 1619 Qy 1475 TCAAGTTCTTCGTTCCACCGTCTCCAGAGGAGCAGCCTGTGGCTTAA 1524 Db 1620 TCAAGTTCTTCCATCCACCGTCTGAACACTCTCAGAGGCTTGGGGCTTTAA 1669	MAY 19312 MAY 19312 MAY 19312 MAY 19313 MAY 19313

65 GGCAGGGGGGGAGGAATGAGTGCCAGTTCCAG		125 ACCGCATTGAGTCTGAGGCGTTALTHITHTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		182 TCTACTCCAATGCTCCCAGGAGATCTTCATCCAGG	245 TCTACTCCAATGCTCCCCTCGAGATCTACGTTCAG	305 TATTCCCTGGTTGTCCTAGTACATATGAGGCCTG	O	365 CCCAAAAGCCATCAAGACGTTTTCAAGTAGGGCAGG 356 ATAGTCACCAGAAGGTGCACCGTTTCGATGAGGGTC 4.5 ATAGTCACCAAAGGTTCAAGAGGTTCAAGAGGTTAAGAGG		485 TIGCTITCIGGAIGIACAACGACGAAGACACTGAIC	476 CCAACAACAACGACAACCTGGTTGATCAGTTCCCC		605 AAGAGCAAGAGTTCTTAAGGTACCAGCAGC	596 CATATAGCCCATACAGCCCGCAAAGTCAGCCTAGAC	635	656 GAGGACAGCAGCGGAGAAACGAAGGAGAAACG	653 ATTATCGACAAATTAGCCCAAGGGTACGAGGTGACC	716 TCTTCAGCGGCTTCACGCGGAGTTCCTGGAACAAC	/ 13 1C11CAGCGC111GCACAGGAG11CC11CAACACC	770 CCGTAGAAATCTTAAGAGGAGAGAGGGGGGGGGGGGGGG	836 GGGGGGCCTCAGAATCTTGAGCCCAGATAGAAA	830 AGGGAGCCTCAGAATCTTAAGCCCAGATGAAGAAC	881 ACGAAGAAGAGAATACGATGAAGATGAATATGAAT	890 gcagacgagadaarrcgargagargagagagagagagagagagagagagag			1001 AAAGAACATIGGTAGAACAGAICCCCTGACATCI 	1061 AAACTGCCAACGATCTCAACCTTCTAATACTTAGG	1067 GAAGCGTCAACGAACTCGACCTCCCAATTCTCGGCT
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CTACAACCCTCAAGCTGGTTCACTCA 1060 AGAGACGATCTGCACCGCAAGTGCTA 1000 TTGGAACCCCAACAACCAGGAGTTCG 121 CCGCCGCATGCCTTCGCAGGCCTT 244 -GAAGACCAAAGCCAACAGCAACGAG 355 TGATCTCATTGCAGTTCCCACCGGTG 415 TGTTGTTGCTGTTTCTCTTACTGACA 475 CAGGAGATTCAATTTGGCTGGGAACA 535 AGAAGAGGAGCCATTGTGACAGTGA 835 GCAAGGAAGGGGATACTTTGGGTTGA 241 TCACACAAGGTCGTCGATCTCAGT 301 CAGACAAAGCAGACGAAGAAGCTTAC 595 AGAAGAAAACGAAGGTGGAAACA 715 AGCCTTCCAGGTTGACGACAGA 775 ATACGATGAAGAGGATAGAAGGCGTG 940 gccacaacaacgregraaaracgare 949 CCGCCGCAACGCCCTTCGTAGGCCTT 181 caddadarrcrarcradccadaaacc 604 634 ACAAGAAGAGCGTGAATTTAGCCCTC 655 ------AGCAAGTAGTCGTCCAC 652 -----GAGACGTGCCG 880 AGATGAGAGCTCGAGGTCGCCTCCCA 889 GCGCCTCAATGCCCAGAGACCCGACA 124

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Pred. No. 5.1e-238;
0; Mismatches 69;
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2872. .3825
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Best Local Similarity 77.1%;
Matches 1233; Conservative
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Arachis hypogaea allergen Arah3/Arah4 gene, complete cds.
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                      GAAATCTCTACAGGAATGCATTGTTTGTCGCTCACTACAACACCAACGCACACACGCATCA 1180
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AL Unpublished
CE 2 (bases 1 to 3825)
DRS Viquez,O.M., Konan,K.N. and Dodo,H.W.
E Direct Submission
UNIVERSITY, Meridian Street, 4900, Normal, AL 35762, USA
Location/Qualifiers
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I. 3825
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join(661. .949,1289. .1581,1669. .2313,2482. .2871)

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1 (Dases 1 to 3825)

Viquez,O.M., Konan,K.N. and Dodo,H.W. Genomic characterization of the major
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SYGLQYEQARQLKNNNPFTFLVPPQDSQMIRTVA"
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Yan, Y., Wang, L. and Huang, S.
Direct Submission
Submitted (30-JUL-2004) Department of Biology and Biotechnology,
Sun Yat-sen University, GuangZhou, GuangDong 510275, China
Location/Qualifiers
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                                    protein gene
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    1786
    organism="Arachis hypogaea"

                                                                                                                                                                                                                                                                                    /note="seed storage protein"
Yan,Y., Wang,L. and Huang,S.
CDNA clone of peanut seed storage
Unpublished
Chases 1 to 1786)
                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:3818"
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Arachis hypogaea
Bukaryota; Viridhjalntae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridhjalntae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Asschynomeneae; Arachis.
1 (bases 1 to 1786)
Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.Z.
Isolation of peanut genes encoding arachins and conglutins by expressed sequence tags
Plant Sci. 169 (2), 439-445 (2005)
2 (bases 1 to 1786)
                                                                                                       AAAACTGCCAACGATCTC----AACCTTCTAATACTTAGGTGGCTTGGACCTAGTGCT
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                                GGCAGGGGAAGCAGGCGGGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGCT
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RESULT 14
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DEFINITION
ACCESSION
VERSION
VERSION
SOURCE
ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE

643 AAGAATTCCTAAGATACCAGCAACGAAGTGGTCGTCAAAGCCCAAAA----

228 181 288 241 348

121

Gaps

141;

Indels

Length 1786;

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/product="de="AaM93157.1"
/db_xref="di="2135348"
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PTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQOSRRR S"

A&M

2. (bases 1 to 657)
Dodo, H. W. and Viquez, O. M.
Direct Submission
Submisted (25-FEB-2002) Food and Animal Sciences, Alabama University, Meridian Street, 4900, Normal, AL 35762, USA Location/Qualifiers

1. .657
/organism="Arachis hypogaea"

/mol_type="mRNA" /db_xref="taxon:3818"

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Ara

Aeschynomeneae; Arachis.

1 (bases 1 to 657)

Dodo,H.W., Viquez,O.M., Maleki,S.J. and Konan,K.N.

cDNA clone of a putative peanut (Arachis hypogaea L.) try
inhibitor has homology with peanut allergens Ara h 3 and
J. Agric. Food Chem. 52 (5), 1404-1409 (2004)

Agric. Food Chem.

14995153

eurosids I; Fabales; Fabaceae; Papilionoideae,

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Match 34.1%; Score 519.2; DB 4; Local Similarity 93.4%; Pred. No. 1.2e-143; es 542; Conservative 0; Mismatches 38;
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02-APR-2004

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mRNA mRNA,

657 bp inhibitor

AF487543 Arachis hypogaea trypsin AF487543

RESULT 15 AF487543 LOCUS DEFINITION

AF487543.1 GI:22135347

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Arachis hypogaea (peanut) Arachis hypogaea Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Nagnoliophyta; eudicotyledons; core eudicotyledons;

Search completed: June 23, 2006, 18:12:43 Job time: 8897.98 secs

Aav17565 Coding se Ab685191 Glycine m Ad489249 G. max gl Ad4313099 Plant ful Adx13099 Plant ful Adx13095 Plant ful Adx13095 Plant ful Adx13098 Plant ful Adx13028 Plant ful Adx13028 Plant ful Adx13028 Plant ful Adx13589 Plant ful Adx13589 Plant ful Adx13589 Plant ful Adx13569 Plant ful Adx1356 Coding se Ad417536 Coding se Ad4189246 G. max gl Adx13060 Plant ful Adx13013 Plant ful

OM nucleic

Run on:

Sequence:

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1. .1524
/*tag= a
/product= "Ara h 3"
/note= "First three amino acids not coded for"
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(UYNY ) UNIV NEW YORK MT SINAI SCHOOL MEDICINE.
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13-FEB-1998;
13-FEB-1998;
13-FEB-1998;
27-AUG-1998;
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   Aaz22280 Ara h 3 a Abx70612 Peanut Ar Adg27543 Peanut Ar Aas08540 DNA encod Aaf90338 Peanut al Abv155193 Glycine m Adh89252 G. max gl Add1997 G. max gl Adx13765 Plant ful Adx1306 Plant ful Adx1306 Plant ful Adx1306 Plant ful Adx13019 Plant ful Adx13019 Plant ful Adx13019 Plant ful Adx13019 Soybean g Adz47105 Soybean g Adz47105 Soybean m Adx47105 Soybean m Adx71010 N-termina
                                                                                                  June 22, 2006, 09:14:45 ; Search time 679.077 Seconds (without alignments) 15647.278 Million cell updates/sec
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              GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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 CAAAACCTAAGGGGGAGACCGAGAGTGAAGAAGAAGGGAGCCATTGTGACAGTGAGGGGA
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                                                                                               This is the nucleotide sequence of the Ara h 3 protein from Arachis hypogea. The Ara h 3 protein has 4 IgE (Immunoglobulin B) binding epitopes, one of which is immunodominant (AAY15281). By modifying the IgE binding sites the ability of the allergen to provoke an immune response is downregulated. The epitopes of the IgE binding sites can therefore be modified in genetically engineered plants and animals to elicit less of an allergic response. (Updated on 17-OCT-2003 to standardise OS field)
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Best Local Similarity 100.0%; Pred. No. 0;
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                       TTCTGGCTCTACAACGACCACGACACTGATGTTGTTGCTGTTTCTCTTACTGACACCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a tertiary structure for the peanut allergen Ara H in The Ara H is allergen is found to contain 23 linear 1gB-binding epitopes. The invention also provides an isolated recombinant peanut allergen designated Ara H 3 and a nucleotide molecule encoding the peanut allergen Ara H 3. Molecules of the invention are used to protect a host animal from allerger reaction, particularly using a modified allergen which is less reactive with IgE. The invention may also be used to ensure that the allergen is not introduced into genetically modified food. The present sequence represents a DNA encoding the Ara H 3 allergen. (Updated on 17-OCT-2003 to standardise OS field)
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/note= "there is an apparent 6 nucleotide deletion which encodes for residues Glu and Phe respectively" /transl except= (pos:1105, .1107, aa:Leu) /product= "that H 3 allergen" /note= "does not encode the first three residues in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 structure of peanut allergen Ara h 1 for protection
                                                                                                                                                                                                                                                                                                                                     elm RM, Cockrell G, Bannon GA, Stanley JS, Sł
Compadre CM, Huang SK, Maleki SJ, Kopper RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1524 BP; 455 A; 390 C; 398 G; 281 T; 0 U; 0 Other;
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                                                                                            corresponding protein sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tertiary structure of peanut a animal from allergic reaction.
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Matches 1524; Conservative
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11-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                        Sampson H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a modified anaphylactic food allergen has an amino acid sequence that is substantially identical to that of natural anaphylactic food allergen, except for a cysteine residue that has been modified so that it cannot participate in the disulphide bond. The modified so that it cannot participate in the disulphide bond. The modified anaphylactic food allergen; (2) a method of making a modified anaphylactic food allergen; (2) a nucleotide molecule encoding or for causing a site specific mutation in the modified anaphylactic food allergen; (3) a transgenic plant or animal expressing the modified anaphylactic food allergen to a natural anaphylactic food allergen is useful for preventing or treating allerger; cand an isolated fragment of peanut allergen anaphylactic food allergen is useful for preventing or treating allergic reactions associated with any natural allergen such as food, insect, treating wounds in mammals such as bovine, canine, feline, captine, cornal, portion, mutating species. The spresent sequence is a CDNA cornal, and the species. The present sequence is a cDNA
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NE, Kopper RA, Maleki SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified anaphylactic food allergen, useful for preventing or treating allergic reactions associated with e.g. anaphylactic allergens.
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                                                                                                                                                                                                                                                                                                                                Peanut, 88; allergy, Ara h1; Ara h2; Ara h3; gene, IgE binding site, anaphylactic food allergen; antiallergenic, vaccine; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 A; 390 C; 398 G; 281 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GA,
King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Helm RM, F
      CAGTCTCCGAGGGCTGTGGCTTAA 1524
                             CAGTCTCCGAGGCTGTGGCTTAA 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 16; Fig 68A; 300pp; English
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                                                                                                                                                             ВР
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                                                                                                                                                             ABX70612 standard; cDNA; 1524
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18-MAR-2002; 2002US-00276822
                                                                                                                                                                                                                                                                                            Ara h3 cDNA sequence
                                                                                                                                                                                                                                               (first entry)
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Rabjohn PA, Shin DS, Sta
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Best Local Similarity 100.
Matches 1524; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PANA-) PANACEA PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sosin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-018765/01.
P-PSDB; ABU52484.
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                                                                                                                                                                                                                                                                                                                                                                                                  Arachis hypogaea
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200274250-A2
                                                                                                                                                                                                                                               26-MAR-2003
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Cockrell G;

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The invention relates to a modified anaphylactic food allergen whose amino acid sequence is substantially identical to that of a natural canaphylactic food allergen. The natural anaphylactic food allergen in a disulphide includes at least one cysteine residue that been modified so that conformation, except that the cysteine residue has been modified so that it cannot participate in the disulphide bond. Also included are a method of making a modified anaphylactic food allergen, a nucleotide molecule conformation a modified anaphylactic food allergen, a transgenic plant or nucleotide molecule for causing a site specific mutation in a gene conformation and anaphylactic food allergen, a transgenic plant or animal expressing a modified anaphylactic food allergen defined above, a conformation and individual by reducing the clinical response to a natural anaphylactic food allergen by administering a modified or anaphylactic food allergen is consecutive amino acids of ADG27464 or ADG27465. About 10-17% of the amino acids have been modified in at least cone IgE epitopes recognised when the natural anaphylactic food allergen is contacted with serum IgE from individual(s) allerger to the natural anaphylactic food allergen and consecutive and consecutive allergen allergen and an isolated fragment of the invention consecutions or consecutive and their encoding consecutives beant allergen and an isolated fragment of the invention discloses Peanut allergens Ara h), Ara h3 (and their encoding consecutions). Soybean Glycinin A2Bla and IgE-binding epitopes of the English and allergen and an individual sequence are anaphylactic good allergen would be an anaphylactic food allergen by a modified anaphylactic food allergen by an under the matural anaphylactic food allergen walnut allergen by an under the anaphylactic food allergen by a modified anaphylactic food
                                                                                                                                                                                                                                         King NE, Kopper RA, Maleki SJ;
                                                                                                                                                                                                                                                                                                                                     New modified anaphylactic food allergen comprising a cysteine residue which has been modified so that it cannot participate in the disulfide bond, useful for treating allergic reactions or wounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGGCAGCAACCGGAGGAGAACGCGTGCCAGTTCCAGCGCCTCAATGCGCAGAGACCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AATCGCATTGAATCAGAGGGCGGTTACATTGAGACTTGGAACCCCAACAACCAGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AATCGCATTGAATCAGAGGGGGGTTACATTGAGACTTGGAACCCCAACAACAGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAATGCGCCGGCGTCGCCTCTCGCTTAGTCCTCCGCCGCAACGCCCTTCGTAGGCCT
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Helm RM, King N
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Best Local Similarity 100.
Matches 1524; Conservative
                                              COCKRELL G.
COMPADRE C M.
CONNAUGHTON C.
                                                                                          HELM R M.
KING N E.
KOPPER R A.
MALEKI S J.
RABJOHN P A.
SHIN D S.
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                  BANNON G A.
                                 BURKS A W.
 SAMPSON H.
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Rabjohn PA,
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(SHIN/)
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(HELM/)
(KING/)
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GAGCAGGCAAGGCAGCTTAAGAACAACACCCTTCAAGTTCTTCGTTCCACCGTCTCAG 1500
                              GCTCACGTGCAAGTCGTGGACAGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG
                                              GCTCACGTGCAAGTCGTGGACAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAG
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                                                                                                                                                           TTCGAATACGTGGCATTCAAGACAGACTCAAGGCCCCAGCATAGCCAACCTCGCCGGTGAA
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                                                                                            GGTCACGTGCTTGTGGTGCCACAGAACTTCGCCGTCGCTGGAAAGTCCCCAGAGCGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peanut; plant; ss; gene; allergen; Ara h1; Ara h2; Ara h3; glycinin A2Bla; Jug n1; antiallergic; vulnerary; anaphylactic food allergen; IgE; allergy; wound.
                                                                                                                                                                                                                                                                                                                                                      CAGTCTCCGAGGCTGTGGCTTAA 1524
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98US-0073283P.
98US-0074590P.
98US-0074624P.
98US-00106872.
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99US-0122565P.
99US-0122566P.
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99US-00240557.
99US-00241101.
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2000US-00494096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arachis hypogaea
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13-FEB-1998;
13-FEB-1998;
29-JUN-1998;
27-AUG-1998;
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02-MAR-1999;
02-MAR-1999;
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29-JAN-1999;
29-JAN-1999;
11-FEB-1999;
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02-MAR-1999
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31-JAN-1998
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The sequence represents the coding sequence of anaphylactic antigen Ara h 3. Ara h 3 is an anaphylactic antigen (A), which was used to design antigenic peptides having a reduced ability to bind immunoglobulin E (1gE) as compared with the intact (A), or having a sequence substantially identical to a portion of sequence of an antigen that includes at least one IgE binding site, where at least one IgE binding site of the peptide is altered. The antigenic peptides are used in a composition which is useful for reducing risk or severity of allergic reaction to an antigen. This is done by identifying an individual at risk of allergic reaction to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigenic fragments useful for reducing anaphylactic risk and reducing the severity and/or number of allergic symptoms in individuals sensitive to antigens, have reduced ability to bind Immunoglobulin E.
                                                                                                               1441 GAGCAGGCAGCTTAAGAACAACCCCTTCAAGTTCTTCGTTCCACGTCTCAG
                      1321 TTCGAATACGTGGCATTCAAGACAGACTCAAGGCCCACCATAGCCAACCTCGCCGGTGAA
                                                                  GAGCAGGCAAGGCAGCTTAAGAACAACAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAG
                                                      AACTCCGTCATAGATAACCTGCCGGAGGAGGTGGTTGCAAATTCATATGGCCTCCAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Peptide antigen Ara h 3"
/note= "Coding sequence of amino acids 1-3 not given"
                                                                                                                                                                                                                                                                                                                            anaphylactic antigen, immunoglobulin E; IgE; immunogenic; mast cell; basophil; mouse; ss.
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UNIV ARKANSAS.
MOUNT SINAI SCHOOL MEDICINE NEW YORK.
                                                                                                                                                                                                                                                                                                       anaphylactic antigen Ara h 3.
                                                                                                                                                  CAGTCTCCGAGGGCTGTGGCTTAA 1524
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                                                                                                                                                                                                                                   AAS08540 standard; cDNA; 1524
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2000US-0213765P.
2000US-0235797P.
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P-PSDB; AAU04708.
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23-JUN-2000;
27-SEP-2000; 2
                                                                                                                                                                                                                                                                                                       DNA encoding
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                                 CAGCACAGCCGCAGAGAACGAGCAGGACAAGAAGAAGAAAAACGAAAGGTGGAAACATCTTC
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                      TCCCAAAGACCACCAAGACGTCTCCAAGGAGAAGACCAAAGCCAACAGCAACGAGTAGT
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an antigen by identifying prior display of allergic symptoms when exposed to the antigen, or a familial relationship with an individual who previously displayed allergic symptoms when exposed to the antigen. Following this an antigen-specific log present on one or more mast cells or basophils in the individual's serum is identified. The individual is then contacted with a peptide corresponding to a portion of the antigen, which is selected, formulated, and delivered so that binding of the peptide to antigen-specific 1gE is reduced as compared with 1gE binding of intact antigen. The composition is also useful for treating and
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                                                                                                          Sequence 1524 BP; 455 A; 392 C; 396 G; 281 T; 0 U; 0 Other;
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Pred. No. 0;
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Matches 1522, Conservative
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/note= "PCR amplified
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1. 1593
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RESULT 7
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                                                                                                                                                                                     The present sequence is that of peanut allergen Ara h3 cDNA. A portion of the Ara h2 gene coding region is homologous to the corresponding region of the peanut allergen Ara h4 gene. This region has been PCR amplified, cloned in transformation vectors (pUCI8 and pB14434) in sense and antisense orientations and used to down-regulate Ara h3 and Ara h4 allergens in peanut. This is an example of the method of the invention, which relates to the production of a peanut plant having reduced, or undetectable, allergenic protein (AP) content in its seed, A peanut plant cell is transformed with a DNA construct containing an antisense AP gene and/or sense AP gene, or their fragments, regenerated to plants, and fertile transgenic plants that produce seeds with reduced AP content are identified. The seeds are useful for preparation of allergen-free foods. (Updated on 11-SEP-2003 to standardise OS field)
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Pred. No. 0;
0; Mismatches
                                                                                   Viquez OM;
                                                                                                                            Producing transgenic peanut plants
useful in non-allergenic foods, by
                                                                                   Konan KN,
                                                                                                                                                                       Claim 20; Fig 4; 72pp; English
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Best Local Similarity 95.4%;
Matches 1454; Conservative C
                     20-NOV-2000; 2000WO-US031657
                                         99US-0167255P
                                                              ALABAMA A & M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the coding sequence for the Gy3 subunit of the soybean seed protein, glycinin. The method of the invention is for reducing the quantity of a soybean seed storage protein (A), such as beta conglycinin, in soybeans. It comprises: (a) constructing a chimeric gene comprising: (i) a nucleic acid fragment encoding a promoter that is functional in the calls of soybean seeds; (ii) a nucleic acid fragment encoding all or a portion of (A) placed in sense or antisense orientation relative to the promoter of (1); and (iii) a transcriptional termination conforms (a) the promoter of (1); and (i) growing the transgenic soybean cell the chimeric gene of (a); where the quantity of one or more members of the chimeric gene of (a); where the quantity of one or more members of a chase of (A) subunits is reduced when compared to soybeans on containing the chimeric gene of (a); where the expression of genes encoding (A) are modulated to soybean lines where the expression of genes encoding (A) are modulated to effect a change in seed storage protein profile of transgenic plants.

Modification of novel soy protein profile can result in the production of novel soy protein profile can result in the profile of transgenic plants.
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Pred. No. 1.7e-137;
0; Mismatches 421; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suppression of specific classes of soybean seed protein genes change seed storage protein profiles of transgenic plants.
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                                                                                                      Gy3 subunit of glycinin.
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protein co-ordinate data; gene;
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                                                                                                                                                                                                                                 AGGCAAGGCAGCTTAAGAACAACACCCCTTCAAGTTCTTCGTTCCACCGTCTCAGCAGT 1504
                                                                                                                                                                                                                                                   ds; gene; double stranded RNA; storage protein; 25-albumen; 75-globulin; 115/125-globulin; zein-prolamine; homogentistate metabolic pathway; pharmaceutical; plant; abiotic stress; fatty acid composition; lipid composition; oil composition; carbohydrate composition; oilour; pigmentation; pathogen resistance; fruit ripening delay; aging; male sterility; lignin; fibre; cotton; Vitamin E synthesis; nicotine; caffeine; theophylline; threonine biosynthesis; glycinin.
 ACGTGCAAGTCGTGGACAGCAACAGAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC
                           regracascreterarrecarrecreaceachererrearceachecrecacheceac
                                                                                     AGGTGTTAATTGTGCCACAAAACTTTGCGGTGGCTGCAAGATCACAGAGCGACAACTTCG
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P-PSDB; ADH89253.
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This invention describes a novel method for reducing the expression of least two different endogenous target genes in a eukaryotic cell or organism by introducing an RNA molecule that is at least partly double stranded. The transcribed RNAs from at least two target genes have homology below 90% and the RNA molecule is formed as a single, self-complementary molecule. At least one of the double-stranded structures

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Control to the RNA molecule may include an intron-encoding sequence. At least two target genes are selected from different classes of storage protein genes, i.e. 25 albumen, 75- or 118/125-globulins or zein-

protein genes, i.e. 25 albumen, 75- or 118/125-globulins or zein-

protein genes, i.e. 25 albumen, 75- or 118/125-globulins or zein-

protein sequences or genes in the homogentistate metabolic pathway or cervity transacylases, thioseterases, (de)branching enzymes types. Genzyme types, e.g. acetyl transacylases, thioseterases, (de)branching enzymes or cellulases. The RNA of the invention, also related cassettes, expression systems, vectors and transgenic organisms are used for preparation of pharmaceuticals, in biotechnological processes and plant confectionly, specifically in plants to improve protection against confection catress, to modify carbohydrate composition, to alter colour or pigmentation, to reduce content of storage proteins, to increase abiotic strass, to modify carbohydrate composition, to alter colour or pigmentation, to reduce content of storage proteins, to increase content of pathogens, to inhibit stem break, to delay fruit ripening or resistance to pathogens, to inhibit stem break, to delay fruit ripening or aging, to induce male sterility, to reduce content of toxic or unwanted components, to modify lightication and/or lighin content, to susceptibility to shock, to increase synthesis of Vitamin E, to reduce contents of nicotine, caffeine or fibophylline and to increase methionine and efficient way of reducing gene expression, can inhibit more then or traget gene, prevente development of multiple phenotypes (since the traget gene, prevente development of multiple phenotypes (since the effective suppression of all target genes), avoids problems of epigenic condition, the method can be applied to plants with complex (polyploid) genomes. On interference between the individual RNA sequences or and the method can be applied to plants with a topic or a target gene is ilenging.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1446 BP; 426 A; 361 C; 354 G; 305 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 517.4; DB 10 Pred. No. 1.7e-137;
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Matches 954, Conservative
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ADG43987 standard; DNA; 1446

RESULT 10 ADG43987 ID ADG4: XX

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This invention describes a novel method for increasing the total oil

content of a plant by reducing the amount of at least one storage protein

to the plant (or its tissue, organs, parts or cells) and selecting plants

that have higher total oil content than starting plants. The storage

that have higher total oil content than starting plants. The storage

protein is suppressed by introducing antisense RNA, optionally combined

with a ribozyme, sense RNA that induces co-suppression. DNA-binding

factors directed against storage protein genes, viral sequences that

degrade storage protein RNA, constructs that induce homologous

combination of endogenous storage protein genes or mutations into

storage protein genes. Most preferably a plant cell is stably transfected

with a recombinant expression construct, then regenerated to plants that

express the incorporated sequence. The expression constructs particularly

contain a seed-specific promorer and they are introduced into plants by

contain a seed-specific promorer and they are introduced into plants by

contain a seed-specific promorer and they are introduced into plants by

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contain a seed-specific promorer and they are introduced into plants or

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contain a seed-specific promorer

contain a seed-specific organisms produced by the new method are used for

production of oils, free fatty acids or their derivatives, useful

contains a storage protein used to illustrate the method of the invention.
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                                                                                                                                     oil content; plant; storage protein; seed-specific promoter; 2S-albumin; Sglobulin; 11S-globulin; 12S-globulin; 2S-albumin; zein-protamine; transgenic; oil production; fat production; free fatty acid production; food; animal feed; pharmaceutical; fine chemical production; ds; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing total oil content of plants, useful e.g. as foods or animal feeds, by reducing amount of storage proteins, particularly with doublestranded interfering RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AGCAGCCACAGCAAAACGAGTGCCAGATCCAACGCCTCAATGCCCTAAAACCGGATAACC
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Pred. No. 1.7
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Best Local Similarity 62.8%;
Matches 954; Conservative
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                                          (first entry)
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P-PSDB; ADG43988.
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1427 AGAGGAGAGTTGTGGCTTA
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05-NOV-2001; 2001US-00985678.
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KOVALIC D K.
SCREEN S E.
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                   AGAAGATCTATCACTTCAGAGGGGGGGTGATTTGATTGCAGTGCCAACCGGTTTTGCATACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
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                                                                                                                                                                                        CCGTCATAGATAACCTGCCGGAGGAGGTGGTTGCAAATTCATATGGCCTCCAAAGGGAGC
AATACGTGGCATTCAAGACAGACTCAAGGCCCAGCATAGCCAACCTCGCCGGTGAAAACT
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           improving plant tolerance to cold, heat, drought, herbidges, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of the
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Pred. No. 1.8e-137;
0; Mismatches 421; Indels 144;
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                     AGGCAAGGCAGCTTAAGAACAACAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAGGGT 1504
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stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of invention.
                                                                                                                                                                       DB 13; Length 1694;
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                                                                                                                            T; 0 U; 0 Other,
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Pred. No. 1.8e-137;
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                         AGTATGTTTCATTCAAGACCAATGATAGACCCTCGATCGGCAACCTTGCAGGTGCAAACT
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the polynucleotide consisting of a sequence encoding an amino acid sequence. The sequence in the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing glactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of the cell cycle by modification of the cell cycle pathway. For conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, introgen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stream of the modifying seed oil or procein yield and/or content. This sequence represents a plant full length insert procein the proportion of the polynucleotide that can be used in the recombinant DNA construct of the
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KOVALIC D K.
SCREEN S E.
                                                                                                                                                                                                           WPI; 2004-180133/17.
                                                                                          TABASKA J E
                                                                                                                                                                 Zhou Y,
                                                                                                                                                                                                                                                                                                                                    improving yield
                                                                                                                   CAO Y.
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                    (ZHOU/)
(KOVA/)
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425 GGCTCTACAACGACCACGACACTGATGTTGCTGTTTCTCTTACTGACACCAACAACA 484

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GGATGTACAACAATGAAGACACTCCTGTTGTTGCCGTTTCTCTTATTGACACCAACAGCT
                                                                                         AGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATATAGCC
                                                                                                                                                                                                                                       CATACAGCCCGCAAAGTCAGCCTAGACAAGAAGAGCGTGAATTTAGCCCTCGAGGACAGC
                                                                                                                                                                                                                                                                                                                                    <u> ACAGCCGCAGAGAACGAGCAGGACAAGAAGAAGAAAACGAAGGTGGAAACATCTTCAGCG</u>
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                                            ACGACAACCAGCTTGATCAGTTCCCCAGGAGATTCAATTTGGCTGGGAACACGGAGCAAG
                                                                                                                                                                                        ATGAATATGAATACGATGAAGAGATAGAAGGCGTGGCAGGGGAAGCAGAGGCAGGGGGA
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at amino acid sequence the sequence. The performance of the invention are also useful in physical arrays of molecules and as plan to breading markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme cosmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of the photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stream of the cell or protein yield and/or content. This sequence represents a plant full length insert content of the cell or protein yield and/or polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; dispasse resistance; yalactomannan production; dispasse resistance; yield; plant growth; plant development; seed oil; protein yield; yield;
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                                    ADX13019 standard; cDNA; 1671
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2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kovalic DK,
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                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                  protein content; gene; ss
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SCREEN S E.
TABASKA J E.
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ZHOU Y.
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                                                                                                                                                                                                                                                                                                                                                     Unidentified.
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05-NOV-2001;
                                                                                                            21-APR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KOVA/)
(SCRE/)
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(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (rin1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZHOU/)
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RESULT 15
ADX13019
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DB 13; Length 1671; T; 0 U; 0 Other;

Score 515.8; DB 13; Pred. No. 5.2e-137;

33.8%; 62.7%;

Best Local Similarity

Query Match

Sequence 1671 BP; 498 A; 404 C; 396 G; 373

Matches	953; Conservative 0; Mismatches 422; Indels 144; Gaps 4;
oy qa	5 AGCAACCGGAGGAGACGCGTGCCCAGTTCCAGGGCTCAATGGGCAGAGACCTGACAATC 64
ò	GCATTGAATCAGAGGGGGGTTACATTGAGACTTGGAACCCCAACAACCAGGAGTTCGAAT
අු ල	GTATAGAGTCAGAAGGTGGCTTCATTGAGACATGGAACCCTAACAACAAGCCATTCCAGT 214
s a	125 GGGCGGGTGCCCTTCTCGCTTAGTCCGCGACGCCTTTCGTAGGCCTTTTT 184 215 GTGCCGGTGTTGCCTCTCTCGCTCAACGCCCTTCGCAGACCTTCCT 274 Db
o S	185 ACTCCAATGCTCCCCAGGAGATCTTCCAGCAAGGAAGGGGATACTTTGGGTTGATAT 244
ò	TCCTGGTTGTCCTAGACACTATGAAGAGCCTCACACACAAGGTCGTCGATCTCAGTCCC
qq	TCCCGGGTTGTCCTAGCACATTTGAAGACCT366
B &	305 AAAGACCACCAAGGACTCTCCAAGGAGAAGACCAACAGCAACGAGATAGTCACC 364 Db 367CAACAAAAAGGACAAAGCAGAGCCCCCAAGACCGTCACC 406
ò	365 AGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTGCAGTTTCCCACCGGTGTTGCTTTCT 424
Db	466
දු පු	425 GGCTCTACAACCACCACCACACTGATGTTGCTGTTTCTTACTGACACCAACAA 484
ò	485 ACGACAACCAGGTTCAGATTCAGATTTGGCTGGGAACACGGGAGCAAG 544
qq	586
Oy Db	545 AGTICTTAAGGTACCAGCAACAAAGCAGACAAGAAGAAGCTTACCATATAGCC 604
ò	CATACAGCCCGCAAAGTCAGCCTAGACAAGAGAGCGTGAATTTAGCCCTCGAGGACAGC
DP	620GAGGTACTC 628
ò 6	665 ACAGCCGCAGAGAACGAGGACAAGAAGAAAAAGGAAGGTGGAAACATCTTCAGCG 724
g ;	Y MANGELAGARANGEMANGELGILAGERANGARAGANGARAH CARAGANGANGANGANGANGALAIAIIIGAGILG
s d	725 GCTTCACGCCGGGAGTTCCTGGAACACCTTCCAGGTTGACGACAGATAGTGGAAA 784
<u>ک</u> ۾	785 ACCTAAGAGGCGAGACCGAGAGGGAGCCATTGTGACAGTGAGGGAGG
& :	TCAGAATCTTGAGCCCAGATAGAAAGAGACGTGCCGACGAAGAAGAAGAATACGATGAAG
<u>a</u> 8	806 TCAGCGTGATAAGCCCACCACGGAAGAGCAGCAAGAGACGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
중 음	A 15 MILL A CARLOAD CARACTER AND
ć	965 ATGGTATTGAAGAGGATCTGCACCGCAAGTGCTAAAAAGAACATTGGTAGAAACAGAT 1024
qa	911 ATGGCATTGACGAGACTTTGCACAATGAGACTTCGCCACAACATTGGCCAGACTTCAT 970
\$ 8	1025 CCCTGACATCTACAACCTCAAGCTGGTTCACTCAAAACTGCCAACGATCTCAACCTTC
	A SAME TO THE SECOND TO THE SE

δ	1085 TAATACTTAGGTGGCTTGGACCTAGTGCTGAATATGGAAATCTCTACAGAAATGCATTGT	GAAATCTCTACAGGAATGCATTGT 1144
qq	1031 CAGCCCTCTCGTGGCTCAAACTCAGTGCCCAGTTTGGATCACTCCGCAAGAATGCTATGT	GATCACTCGCAAGAATGCTATGT 1090
ò	1145 TIGICGCTCACTACAACACCAACGCACACACATCATATATCGATTGAGGGGACGGCTC	TATATCGATTGAGGGGACGGCTC 1204
qq	1091 TCGTGCCACACTACAACCTGAACGCAAAATATATACGCATTGAATGGACGGCAT	
٥٨	1205 ACGTGCAAGTCGTGGACAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC	ACGACGAGGAGCTTCAAGAGGGTC 1264
Db	1151 TGGTACAAGTGGTGAATTGCAATGGTGAGAGTGTTTGATGGAGAGCTGCAAGAGGGAC	TTGATGGAGAGCTGCAAGAGGGAC 1210
ò	1265 ACGTGCTTGTGGTGCCACAGAACTTCGCCGTCGCTGGAAAGTCCCAGAGCGAGAACTTCG	GAAAGTCCCAGAGCGAGAACTTCG 1324
Ob	1211 AGGTGTTAATTGTGCCACAAAACTTTGCGGTGGCTGCAGAGATCACAGAGCGACAACTTCG	GAAGATCACAGAGGGACAACTTCG 1270
ò	1325 AATACGTGGCATTCAAGACAGACTCAAGGCCCAGCATAGCCAACCTCGCCGGTGAAAACT	TAGCCAACCTCGCCGGTGAAAACT 1384
Dp	1271 AGTATGTTTCATTCAAGACCAATGATAGACCCTCGATCGGAACCTTGCAGGTGCAACT	TCGGCAACCTTGCAGGTGCAAACT 1330
ò	1385 CCGTCATAGATAACCTGCCGGAGGAGGGGTTGCAAATTCATATGGCCTCCAAAGGGAGC	ATTCATATGGCCTCCAAAGGGAGC 1444
Dp	1331 CATTGTTGAACGCATTGCCGGAGGAAGTGATTCAGCAAACTTTTAACCTAAGGAGGCAGC	AAACTTTTAACCTAAGGAGGCAGC 1390
λ̈́o	1445 AGGCAAGGCAGCTTAAGAACAACAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAGCAGT	TCTTCGTTCCACCGTCTCAGCAGT 1504
Dp	1391 AGGCCAGGCAGGTCAAGAACAACACCCTTTCAGCTTCCTGGTTCCACCTAAGGGGTCTC	TCCTGGTTCCACCTAAGGGGTCTC 1450
ò	1505 CTCCGAGGCTGTGGCTTA 1523	
qa	1451 AGAGGAGATTGTGGCTTA 1469	
Search c	Search completed: June 22, 2006, 11:35:36	

Search completed: June 22, 2006, 11:35:36 Job time : 691.077 secs

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EST531320 EST635105 EST635685 EST635507

EST531229 EST609649

EST635708

EST635674

EST608905

EST635650 EST636071

EST531305 EST531323

EST636033

EST635979 EST635152 EST608926

UTPPI009

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Arachis hypogaea (peanut)

Bukaryorda, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryorda; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;

Aschymoneneae; Arachis.

Loo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.

and Lymch,R.E.

Generation and Analyses of ESTs for Arachis hypogaea

Unpublished (2003)

Contact: Baczhu Guo

Molecular Generics
USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd., Tifton, GA 31794, USA

Tel: 229-387-2321

Email: bguo@tifton.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lab_host="XL1-blue"
clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD018329
UTPP1007_B05 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPP1007_B05 5', mRNA sequence.
CA857935
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/clone="UTPP1007 B05"
/tissue_type="lmmature pods"
/dev_stage="R6"
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                               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -800C freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIRCOREL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were
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(UIPP) (ADDA IDEAD YR, Site 1: ECORI; Site 2: XhoI; CONA library was constructed from peanut cultivar Al3 (NOVINTARA) as a resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -800C freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(SIBCOBRI). mRNA was extracted and purified from ultrapuretion followed the protocol of by ZAP-CDNA Gigapack total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Unit-ZAP XR vector using XhoI ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Unit-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                                                                                                                                               Arachis hypogaea (peanut)
Arachis hypogaea
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                    CD038327 17-MAY-2)
UTPP1008_F09 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPP1008_F09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 725)
Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGCAGCAACCGGAGGAACGCGTGCCAGTTCCAGCGCCTCAATGCGCAGAGACCTGACA
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USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA
1229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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/tissue_type="Immature pods"
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/lab_host="XL1-blue"
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/cultivar="A13"
                                                                                                                                                                                                                                                                                                                                                                               Aeschynomeneae; Arachis.
1 (bases 1 to 725)
                                                                                                                                               CD038327
CD038327.1 GI:30420165
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match 36.9%; Score 562.2; DB 4;
Best Local Similarity 92.2%; Pred. No. 1.2e-143;
Matches 630; Conservative 0; Mismatches 38;
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Arachis hypogaea cDNA clone UTPP1004_F06 5', mRNA sequence.
CD038254 1 G1:30420092
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                                                                                                                                                                                  CCCAAAGACCACCAAGACGTTTTCAAGGACAAGACCAAAGACCAACAGCAACAGGATAGTC 396
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Wharryca, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae,
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1 (bases 1 to 676)
Luo, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G. and Lynch, R.E.
                                                                                                                         AAGAGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGAGGAGAAGAAGCTTACCATATA
                                                                                                                                                                                                                                                                                                                                                                                                            GCCCATACAGCCCGCAAACTCAGCCTAAACAAGAAGACCGTGAATTTAGCCCTCGAGGAC
                 AATGCGCCGGCGTCGCCCTCTCGCGCTTAGTCCTCCGCCGCAACGCCCTTCGGAGGCCTT
                                                                                rchácticcaargereceaggagarerrearceaggaggaaggggaraerrregarrea
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                                                      ACAACGACAACCAGCTTGATCAGTTCCCCAGGAGATTCAATTTGGCTGGGAACACGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and Analyses of ESTs for Arachis hypogaea Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, CGORECTION and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           669
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/mol_type="mRNA"
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Email: bguo@tifton.usda.gov
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/OCCE="Vector: Uni-ZAP XR; Site 1: ECORI; Site 2: XhoI; CDNA library was constructed from peanut cultivar Al3 (NCVIIXARA). Al3 has resistence to Appergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liguid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRI). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamma library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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/db_xref="taxon:3818"
/clone="UTPP1004" F06"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_host="XL1-blue"
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CD038332 T1fton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPP1004_B04 5', mRNA sequence.
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Arachis hypogaea, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Stermatophyta; Magnoliophyta; eudicotyledons;
Tosids; eurosida I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
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                                                                                   241 TGCATTGAGGGGACGGGCTCACGTGCAAGTCGTGGACAGCAACGGCAACAGAGTGTACGA
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USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
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Contact: Baozhu Guo
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/cultivar="A13"
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                                                                                                                                                                                                                                               CD038107 110 bp mRNA linear EST 07-MAY-2003 UTPP1002_E08 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPP1002_E08 5', mRNA sequence.
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    directionally closed into Uni-ZAP XR vector using Xhol BCoRI sites adapters. The landa library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Labrary
                            594 AGGAATGCATTGTTGTCCCTCACTACAACACAGAACGCACAGCATCATATATGCATTG 653
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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/lab_host="XII-blue"
/clone lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
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1 (bases 1 to 710)
Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and Analyses of ESTs for Arachis hypogaea Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPP1002_E08"
/tissue_type="Immature_pods"
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                                                                                          1192 AGGGGACGGGCTCACGTGCAAGT 1214
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                                                                                                                    654 AGGGGACGGCTCATGTGCAAGT
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Arachis hypogaea
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Matches 571; Conservative
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Email: bquo@tiftor
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p mRNA linear EST 13-AUG-2004
library Arachis hypogaea cDNA 5',
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Varidiplantae; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.
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Yan, Y. S., Wang, L., Zhong, Y. J. and Huang, S. Z.
Yan, Y. S., Wang, L., Zhong, Y. J. and Huang, S. Z.
Expressed sequence tags of mid-matured cotyledons of peanut
Unpublished (2004)
Contact: ShangZhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology
GuangZhou, 510275, China
Tel: (860)02084036592
Email: yys980303wahoo.com.cn
Seq primer: pTriplez Forward.
Location/Qualifiers
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/tissue_type="Cotyledons"
/dev_stage="Mid-matured stage"
/lab_host="E.coli BM25.8"
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/cultivar="Yueyou 523"
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EST00001 Peanut Lambda Express
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Arachis hypogaea
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Best Local Similarity 93.6
Matches 508; Conservative
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CO897496
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                                                                                                                                                     /UDIDE="Vector: Uni-ZAP XR; Site 1: ECORI; Site 2: Xhol; CDNA library was constructed from peanut cultivar All (NCVIIXARA) all has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack II Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using Xhol ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                          clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 CCGGGAGGAGGTGGTTGCAAATTCATATGGCCTCCCAAGGGAGCAGGCAAGGCAGCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.0%; Score 548.6; DB 4; Length 718; larity 93.4%; Pred. No. 7.3e-140; Conservative 0; Mismatches 29; Indels 15.
                    /clone="UTPP1004_B04"
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/dev_stage="R6"
/lab_host="XL1-blue"
db xref="taxon:3818"
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Best Local Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
                                                                                                                                                                                                                                                                                                                                                  120
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UTPPI004 B11 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPPI004_B11 5', mRNA sequence.
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Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davvis Rd., Tifton, GA 31794, USA
Fax: 229-387-2321
Email: bguo@cifton.usda.gov
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                                                                                                                                                                                                            1057 CTCAAAACTGCCAACGATCTCAACCTTCTAATACTTAGGTGGCTTGGACCTAGTGCTGAA
                                                                                                                                                                                                                                                                                                                             61 TATGGAAATCTCTACAGGAATGCATTGTTTGTCCCTCACTACAACACACGAACGCACACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                           1237 GTGTACGACGAGGAGCTTCAAGAGGGTCACGTGCTTGTGGTGCCACAGAACTTCGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1417 GCAAATTCATATGGCCTCCAAAGGGAGCAGGCAAGGCAGCTTAAGAACAACAACCCCTTC
                                                                                                                                                                                                                                                     1 crcaaaacrgccaacgagcrcaaccrrcraarccrraggrggcrrggacrragrgcrgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1357 AGCATAGCCAACCTCGCCGGTGAAAACTCCGTCATAGATAACCTGCCGGAGGAGGTGGTT
                                                                                                                                                                   Gaps
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                                                                                                                     Length 602;
                                                                                                                                                                 20; Indels
                                                                                                                     Score 436; DB 4; I
Pred. No. 9.1e-109;
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                                                                                                                   Query Match 28.6%; Score 436; DB Best Local Similarity 95.7%; Pred. No. 9.1e Matches 448; Conservative 0; Mismatches
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Arachis hypogaea
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosida; eurosida I; Fabales; Fabaceae; Papilionoideae;

Aeschynomeneae; Arachis.

Aeschynomeneae; Arachis.

Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.

Generation and Analyses of ESTs for Arachis hypogaea

L Unpublished (2003)

Contact: Baozhu Guo

Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd., Tifton, GA 31794, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD038301 602 bp mRNA linear EST 07-MAY-2003 UTPP1005_C08 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPP1005_C08 5', mRNA sequence.
                                                                          420
                                                                                                                        518
                               TGCAGTTCCCACCGGTGTTGCTTTCTGGCTCTACAACGACCACGACACTGATGTTGTTGC 458
                                                                                                                                                CAATITIGGCIGGGAACACGGAGCAAGAGITCTIAAGGIACCAGCAACAAAGCAGAAAG 578
                                                                                                                                                                                                                                             /tissue_type="Immature pods"
/dev_stage="R6"
/lab_host="XI-blue"
/clone_lbe="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
                                                                                                                   TGTTTCTTACTACCAACCAACAACGACAACCAGCTTGATCAGTTCCCCAGGAGATT
                                                       /organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3818"
/clone="UTPP1005_C08"
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Location/Qualifiers
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CD038301.1 GI:30420139
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FEATURES

Arachis hypogaea Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.

Arachis hypogaea (peanut)

Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.

Generation and Analyses of ESTs for Arachis hypogaea Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321

/organism="Arachis hypogaea" /mol_type="mRNA" /cultivar="Al3"

Location/Qualifiers

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ORGANISM
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AUTHORS
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(NOTOTE="Wector: Uni-ZAP XR; Site 1: ECORI; Site 2: Xhol;

CDNA library was constructed from peanut cultivar All

(NCVITARAH) all has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -800c freezer.

Total RNA was isolated with TRIZOL-Reagent
ultrapure (ISECORE). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-CDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using Xhol
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phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1265 ACGTGCTTGTGGTGCCACAGAACTTCGCCGTCGCTGGAAAGTCCCAGAGCGAGAACTTCG 1324
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                                                                                        /dev_stage="R6"
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/clone llb="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TAATCCTTAGGGGCTTGGACTTAGTGCTGAATATGGAAATCTCTACAGGAATGCATTGT
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/tissue_type="Immature pods"
                             'db xref="taxon:3818"
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/ OTCE="Vector: Uni-ZAP XR; Site 1: ECORI; Site 2: Xho!; CDNA library was constructed from peanut cultivar Al3 (NCVLIXAR4). Al3 has resistance to Appergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (SIECOBRL). mRNA was extracted and purified from total RNA (Promega). CDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack II Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to exise pBluescript phagemids from the Uni-ZAP XR vector; and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                                                                        /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
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/db_xref="taxon:3818"
/clone="UTPP1001_F09"
/tissue_type="Immature_pods"
/dev_stage="R6"
/lab_host="XL1-blue"
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Best Local Similarity 96.8
Matches 394; Conservative
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CD038043 17-20 bp mRNA linear EST 07-MAY-2003 UTPP1001_F09 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP) Arachis hypogaea cDNA clone UTPP1001_F09 5', mRNA sequence.

CD038043 CD038043.1 GI:30419881

ACCESSION VERSION

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JULEAN JULIAN TO STAP XR, SITE 1: ECORI; SITE 2: XhOI; CDNA library was constructed from peanut cultivar Al3 (NCVIIXAR4). Al3 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-CDNA Gigapack II Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI ECORI sites adapters. The lamda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."
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                                                                                                                                                                                                                418
                                                                                                                                                                                                                                                 369 GTCACCAGAAAGTGCGCCGTTTCGATGAGGGTGATCTCATTGCAGTTCCCACCGCTGTTG 428
249 TATTCCCTGGTTGTCCTAGCACATATGAAGAGCCTGCACAACAAGGTCGCCGGCATCAGT 308
                                                                                                                                     Eukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
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(UTPP)"
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                                                                                                                                                                                                            359 GTCACCAGAAGGTGCACCGTTTCGATGAGGGTGATCTCTTTGCAGTTCCCACCGGTGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                      CTCTCTGGATGTACAACGACCATG 452
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/clone="UTPP1003_A11"
                                                                                                                                                                                                                                                                                                                                                             419 CTTTCTGGCTCTACAACGACCACG 442
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/lab_host="XL1-blue"
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/cultivar="A13"
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Arachis hypogaea (peanut)
Arachis hypogaea
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CD038144
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.

SE Yan, Y.S., Wang, L., Zhong, Y.J. and Huang, S.Z.
Expressed sequence tags of mid-matured cotyledons of peanut
Unpublished (2004)
Context: Shangzhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology
Guangzhou, 510275, China
Tel: (860)02084036592
Email: Yys980304yahoo.com.cn
Seq primer: pTriplEx2 Forward.

Seq primer: pTriplEx2 Forward.
                                                                                                                                             1418 CAAATTCATATGGCCTCCAAAGGGAGCAGGCAAGGCAGCTTAAGAACAACAACAACCCTTCA 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CO897497 452 bp mRNA linear EST 13-AUG-2004 EST00002 Peanut Lambda Express library Arachis hypogaea cDNA 5',
   GCATAGCCAACCTCGCCGGTGAAACTCCGTCATAGATAACCTGCCGGAGGAGGTGGTTG 1417
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                                                                                                                                                                                             301 CAPATICATATGGCCTCCCCAAGGGAGCAGGCAAGGCAGCTTAAGAACAACAACCCTTCA 360
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24.5%; Score 373.6; DB 8; Length 452;
Best Local Similarity 91.7%; Pred. No. 1.5e-91;
Matches 407; Conservative 0; Mismatches 34; Indels 3
                                                                                                                                                                                                                                                                                      1478 AGTICTICGITCCACCGICTCAGCAGTCTCCGAGGGCTGTGGCTTAA 1524
                                                                                                                                                                                                                                                                                                                               361 AGTTCTTCGTTCCACCTTTTCAGCAGTCTCCGAGGGCTGTGGCTTAA 407
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/dev stage="Mid-matured stage"
/lab_host="E.coli BM25.8"
/clone lib="Peanut Lambda Express library"
/note="Organ: Seed; Vector: lambdaTriplEx2"
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/mol_type="mRNA"
/cultivar="Yueyou 523"
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/clore lib="GLSD"
/clore lib="GLSD"
/note="Wettor: pBluescript SK-; Site_l: EcoRI; Site_2:
Xhol; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. CDNA was prepared from polyA+ enriched RNA.
The CDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1214 TCGTGGACAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTCACGTGCTTG 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 TCTTGGAAGATGCATTGAACGTGA---ACAGGCATATAGTTGAAAAAACTTCAAGGCAGGA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 gaggaaggaacaacaagaarargaaggaaggcaacarrrrcagrggcrrcaagagggarr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 ATGAGTGGAGGCCACATCATCAGAAAAGCAGAAAGAGAAAAGAGAAAGGCACAACGGTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        974 AAGAGACGATCTGCACCGCAAGTGCTAAAAAGAACATTGGTAGAAACAGATCCCCTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 CGGAAACAATTTGCACTGCCAGGCTTCACCAGGAACATGGTCTCATCTTCATCACGTGACA
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                                                                                                                                                                                                                                                                                                                                                                                   Length 906;
                                                                                                                                                                                                                                                                                                                                                                                   ch 21.7%; Score 330.4; DB 3; Length 11 Similarity 63.5%; Pred. No. 1.6e-79; 540; Conservative 0; Mismatches 301; Indels
  /lab host="XLOLR"
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Best Local S:
Matches 540
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EST608985 GLSD Medicago truncatula cDNA clone pGLSD-32121, mRNA
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosida I, Pabales, Fabaceae, Papilionoideae, Trifolieae,
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TIGR sequence name: MTRAQS9TK More information is available at:
                                                                                                                                                                                         ccreagecrecagaarregecaceagegegaargecarrerrereccercacracaacace
                                                                                                                                                                                                                                                                  1225 AACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTCACGTGCTTGTGGGTGCCACAG
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                                                                                                                                            AACGCACACACACCATCATATATCGATTGAGGGACGGGCTCACGTGCAAGTCGTGGACAGC
                                                                                               Gaps
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ESTs from late stage developing seeds of Medicago truncatula Unpublished (2002)
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                                                  Length 679
                                                                                               30; Indels
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USDA/ARS Children's Nutrition Research Center
USDA/ARS Children's Nutrition Research Center
BAJOr College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
                                             Score 372; DB 4;
Pred. No. 4.6e-91;
0; Mismatches 30;
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/clone="pGLSD-32121"
/tissue_type="Immature seeds"
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primer. Skmod (CTA gAA CTA gtg
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Location/Qualifiers
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/cultivar="A17"
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BQ123409.1 GI:20175371
                                               24.4%;
92.9%;
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                                             Query Match 24.4
Best Local Similarity 92.9
Matches 390; Conservative
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DEFINITION
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JOURNAL
COMMENT
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KEYWORDS
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CABS/975
BST635230 GLSD Medicago truncatula CDNA clone pGLSD-26J23, mRNA sequence.
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Medaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                       219 ATGAAGACCAGGAGAAAGGAGCCATTGTCAAAGTGGAAGGAGGACTCAGCATCATGAGCC
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                            of Medicago truncatula
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ESTs from late stage developing seeds of Medicago truncatula Unpublished (2002)
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USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
100 Bates Street, Houston, TX 77030-2600, USA
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/clone libe Gibbs.
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xho!; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. cDNA was prepared from polyA+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                           BQ123283 974 bp mRNA linear EST 17-APR-2002 EST608859 GLSD Medicago truncatula cDNA clone pGLSD-31N1, mRNA
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
TIGR sequence name: WTRAO73TK More information is available at:
www.medicago.org
seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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ESTs from late stage developing seeds of Medicago truncatula Unpublished (2002)
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/tissue_type="Immature seeds"
/dev_tstage="25 to 35 days after pollination"
/lab_host="XLOLR"
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USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
111 713 798 7044
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/cultivar="A17"
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XhoI; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. cDNA was prepared from polyA+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
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EST635747 GLSD Medicago truncatula cDNA clone pGLSD-38K19, mRNA
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Cheung, F. and Fraser, C.M.
Cheung, F. and Fraser, C.M.
Unpublished (2002)
Contact: Grusak, M.A.
Contact: Grusak, M.A.
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Fax: 713 798 7078
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/tissue_type="Tmmature seeds"
/dev_stage="25 to 35 days after pollination"
/lab_hose="XLOLR"
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More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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XhoI; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. cDNA was prepared from polyA+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Glapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 TCTACAACCCTCAAGCTGGTAGAATCAAAACTATCACCAGCTTCGACCTCCCAGCTCTCA 456
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                                                                                                                                                                                                                                                                                                                                                                                  /dev stage="25 to 35 days after pollination"
/lab_host="XLOLR"
Tel: 713 798 7044

Fax: 713 798 7078

Email: mgrusak@bcm.tmc.edu

TIGR sequence name: MTRBM60TK

More information is available at: www.medicago.org

Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

Location/Qualifiers
                                                                                                                                                                                                                        /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                               /clone="pgLSD-26J23"
/tissue_type="Immature seeds"
                                                                                                                                                                                                                                                                                                           db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="GLSD"
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were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                    105 TCTTGGAAGATGCATTGAACGT---GAACAGGCATATAGTTGAAAAACTTCAAGGCAGGA
                                                                                                                                                                                                                        TGGTGCCACAGAACTTCGCCGTCGCTGGAAAGTCCCAGAGCGAGAACTTCGAATACGTGG
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                                                                          Gaps
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                                                cch 20.6%; Score 314; DB 4; Length 861; al Similarity 64.0%; Pred. No. 5.4e-75; 525; Conservative 0; Mismatches 285; Indels
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Sequence 11, Appl
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                                                                    June 23, 2006, 09:43:18; Search time 237.534 Seconds (without alignments) 12004.877 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                          'EMG_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

'EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

'EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

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'EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

'EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                                                                                                                                                l cggcagcaaccggaggagaa......tcccgagggctgtggcttaa 1524
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Sequence 13,
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-108-108-13
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US-09-108-1018-12
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US-09-108-1018-14
US-09-788-65-15
US-09-108-1018-14
US-09-788-65-15
US-09-108-1018-14
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114.6 1018.6	US-08-626-554-2	US-09-149-310-38	US-09-645-593-8	US-08-232-463-14	US-09-462-720-3	US-09-949-016-13584	US-09-949-016-13042	US-09-007-005-17	US-09-244-796-17	US-09-949-016-14193	US-09-949-016-13840	US-08-688-376-1	US-08-772-440-33	US-09-949-016-13032	US-09-671-317-14	US-09-671-317-439	US-08-676-967-2	US-08-676-974-2	US-09-098-487-2	US-09-949-016-14543	US-09-949-016-12557	09-396-985B-4
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APPLICANT: DODO, HORTENSE W.
APPLICANT: ARNYZEN, CHARLES J.
APPLICANT: KONAN, KOFFI N'DA
APPLICANT: WOMEN KOFFI N'DA
TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
TITLE OF INVENTION: TRANSCRIC PEANUT SEEDS
TITLE OF INVENTION: TRANSCRIC PEANUT SEEDS
FILE REFERENCE: 072121/0104
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/167,255
PRIOR APPLICATION NUMBER: 60/167,255
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 4
LENGTH: 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AATGCGCCGGCGTCGCCTCTCGCTTAGTCCTCCGCCGCAACGCCCTTCGTAGGCCTT 181
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Pred. No. 0;
0; Mismatches
ALIGNMENTS
                                                                                                            Sequence 4, Application US/09715036
Patent No. 6943010
GENERAL INFORMATION:
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Best Local Similarity 95.4%;
Matches 1454; Conservative
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                                      71 AGCAGCCACAGCAAAACGAGTGCCAGATCCAACGCCTCAATGCCCTAAAACCGGATAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEMOURS AND
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WOND 7.0A
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/09/108,010B
FILING DATE: 30-JUN-1998
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                            1570 CAGTCTCCGAGGCTGTGGCTTAA 1593
                                                                                                                                                                      CAGTCTCCGAGGCTGTGGCTTAA 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09108010B
Patent No. 6362399
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. D
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Matches 954; Conservative
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TATTCCCTGGTTGTCCTAGCACATATGAAGAGCCTGCACAACAAGACGCCGCGATATCAGT 370
                                                                        371 CCCAAAGACCACCAAGACGTTTGCAAGAAGAAGACCAAAGCCAACAGCAACAGATAGTC 430
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                                                                                                                ACCAGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTGCAGTTCCCACCGGTGTTGCTT
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TGGTACAAGTGGTGAATTGCAATGGTCAGAGAGTGTTTGATGAGAGACTGCAAGAGGGGAC 1186
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                                                                                                                   1187 AGGIGITAATIGIGCCACAAAACTITGCGGIGGCIGCAAGAICACAGAGGGACAACTICG 1246
                                                                                                                                                                                                                                                                CCGTCATAGATAACCTGCCGGAGGAGGTGGTTGCAAATTCATATGGCCTCCAAAGGGAGC 1444
                                                                                                                                                                                                                                                                                                                                                                                                1367 AGGCCAGGCAGCTCAAGAACAACAACCCTTTCAGCTTCCTGGTTCCACCTAAGGAGTCTC 1426
                                                                                                                                                                                                                                                                                                                                                           1445 AGGCAAGGCAGCTTAAGAACAACAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAGCAGT 1504
                                                                                                                                                                  1325 AATACGTGGCATTCAAGACAGACTCAAGGCCCAGCATAGCCAACCTCGCCGGTGAAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 517.4; DB 3;
Pred. No. 2.9e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ANTHONY JOHN KINNEY
APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROESOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/09/758,652
FILLING DATE: 11-Jan-2001
CLASSIFICATION: <universely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,971
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFRAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 13
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Patent No. 6703544
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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Best Local Similarity
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US-09-758-652-13
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GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROFSOFT WORD 7.0A
CURRENT APPLICATION NOMBER: US/09/108,010B
FILING DATE: 30-Jun-1998
CLASSIFICATION: <UNKNOWN>
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                        ENGE CHARACTERISTICS:
LENGTH: 1446 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                    34.0%;
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STRETT: 1007 MARKET STREET
STATE: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
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Patent No. 6703544
GENERAL INFORMATION:
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Pred. No. 5.5e-138;
0; Mismatches 425; Indels 150;
               APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-108-010B-11
                                                                                                              TELECOMMUNICATION INFORMATION
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
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SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
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62.7%;
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Matches 968; Conservative
   APPLICATION
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Patent No. 6628491
GENERAL INFORMATION:
APPLICANT: ANTHONY JOHN KINNES
GENERAL GARY MICHAEL FADER
GARY MICHAEL FADER
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Pred. No. 5.5e-138;
0; Mismatches 425; Indels 150;
                                                    95
             MEDIUM TYPE: DISKETTE, 3.50 INCH COMPOUTER: LEB PR COMPATIELE BOPERATING SYSTEM: MICROSOFT WINDOWS SOFTWARE: MICROFSOFT WORD 7.0A
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTBHBURY
REGISTRATION NUMBER: 30, 971
REFERENCE/DOCKET NUMBER: BB-1071-A
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                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11.Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                              APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
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Local Similarity 62.7%;
les 968; Conservative
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Best Local S:
Matches 968
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Pred. No. 5.5e-138;
0; Mismatches 425; Indels 150;
                                                                                                                                                                                                        ADDRESSEE: B. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROFSOFT WORD 7.0A
CURRENT APPLICATION DATA:
PILING DATE: 14-0ct-2003
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION TO COMMUNICATION APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTOREY AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
                                                                                                                                                                                                                                                                                                                                                      STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA
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MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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Best Local Similarity 62.7
Matches 968; Conservative
    INVENTION:
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                                             CATACAGCCCGCAAAGTCAGCCTAGACAAGAAGAGCGTGAATTTAGCCCTCGAGGACAGC
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US-09-805-694B-15
Sequence 15, Application US/09805694B
Patent No. 6864362
GENERAL INFORMATION:
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                                                                                                   Sequence 1, Application US/09762381

Patent No. 6576820

GENERAL INFORMATION:
APPLICANT: TAKAIWA, Fumio
APPLICANT: TUtsumi, Shigeru
APPLICANT: TUtsumi, TRANSCRNIC PLANT EXPRESSING SOYBEAN GLYCININ
TITLE OF INVENTION TRANSCRNIC PLANT EXPRESSING SOYBEAN GLYCININ
FILE REFERENCE: 201487/1050
CURRENT PILLOATION NUMBER: DS/09/762,381
CURRENT PILLOG DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1998-03-04
PRIOR FILING DATE: 1998-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.7%; Score 513; DB 3; Length 1743; 62.7%; Pred. No. 6e-138; ive 0; Mismatches 425; Indels 150;
                TCTTCGTTCCACCGTCTCAGCAGTCTCCGAGGGCTGTGGCTTA
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 62.7
Matches 968; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (52)..(1536)
US-09-762-381-1
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                                    TCAGAATCTTGAGCCCA-----GATAGAAAGAGACGTGCCGACGAAGAAGAAGAAT
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ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
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APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SOYBEAN SEED
PROTEIN GENES
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
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US-09-108-010B-12
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APPLICANT: Kinney, Anthony
TITLE OF INVENTIVO: Hypoallergenic Transgenic Soybeans
FILE REFERENCE: BB1432 US NA
CURRENT APPLICATION NUMBER: US/09/805,694B
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/189,823
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97
SEQ ID NO IS
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Pred. No. 1.2e-135;
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Best Local Similarity 62.4%;
Matches 963; Conservative
                                                                                                                                                                                              TYPE: DNA
CORGANISM: Glycine max
US-09-805-694B-15
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APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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US-09-758-652-12
; Sequence 12, Application US/09758652
; Patent No. 6703544
; Patent No. MARMATION:
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CORRESPONDENCE ADDRESS:
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Pred. No. 2.2e-135;
0; Mismatches 450; Indels 129;
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                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,010B
FILING DATE: 30-Jun-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBRY
REGISTRATION NUMBER: 30,971
REPERRENCE/DOCKET NUMBER: BB-1071-A
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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TOPOLOGY: linear
;
MOLECULE TYPE: CDNA
;
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-108-010B-12
SOFTWARE: MICROFSOFT WORD 7.0A
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SEQUENCE CHARACTERISTICS:
LENGTH: 1458 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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62.0%;
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Best Local Similarity 62.0
Matches 943; Conservative
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                                  AGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATATAGCC
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Pred. No. 2.2e-135;
0; Mismatches 450; Indels 12
     COMPANY
     PONT DE NEMOURS AND
                                                                                                                       MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROFOST WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
MATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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                                                                       COUNTRY: UNITED STATES OF AMERICA ZIP: 19898
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/019,940
FILING DATE: UNDE 14,1996
ATTORNEY/AGENT INFORMATION:

NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
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SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-758-652-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1458 base pairs
STREET: 1007 MARKET & CITY: WILMINGTON STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 62.0%;
Matches 943; Conservative
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Pred. No. 2.2e-135;
0; Mismatches 450; Indels 129;
                                                                                                                                                                                                                                STREET: 1007 MARKET STREET
CITY: WILMINGTON
STAFF NOT THE STREET
                                                                    APPLICANT: ANTHONY JOHN KINNEY
APPLICANT: GARY MICHAEL FADER
TITLE OF INVENTION: SUPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROFSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/684,651
FILING DATE: 14-Outhown.
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UNITED STATES OF AMERICA ZIP: 19898
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SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-684-651-12
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TELEPHONE: 302-992-5481
Sequence 12, Application US/10684651
Patent No. 6828491
GENERAL INFORMATION:
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LENGTH: 1458 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 12:
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STRANDEDNESS: single
TOPOLOGY: linear
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62.0%;
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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Best Local Similarity 62.03
Matches 943; Conservative
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Pred. No. 1e-46;
0; Mismatches 600; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         AL INFORMALLOW:
APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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APPLICATION NUMBER: 60/019,940
FILING DATE: UNNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REGISTRATION NUMBER: 30,971
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROFSOFT WORD 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/108,010B
FILING DATE: 30-Jun-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UNITED STATES OF AMERICA
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SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                   1436 CTCAGAGGAGAGCTGTGGCTTA 1457
                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/09108010B Patent No. 6362399 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1551 base pairs
                                                                                                                                         AGTCTCCGAGGGCTGTGGCTTA
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INFORMATION FOR SEQ ID NO: 15:
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STRANDEDNESS: single
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Best Local Similarity 51.4%;
Matches 699; Conservative
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Pred. No. 1e-46;
0; Mismatches 600; Indels
                                                                                                                                                                                                                                                                                                                                                                                      PONT DE NEMOURS AND COMPANY
                                                                                      GGGAGAACAAGGATTGGAATATGTAGTGTTCAAGACACAC 1410
                                                        1308 CCAGAGCGAGAACTICGAATACGTGGCATTCAAGACAGAC
                                                                                                                                                                                                                                              APPLICANT: ANTHONY JOHN KINNEY
APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROFSOFT WORD 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: LYNNE M. CHRISTENBURY
REGIGSTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
CLASSIFICATION: <Unknown>
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MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: JUNE 14,1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        Sequence 15, Application US/09758652
Patent No. 6703544
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1551 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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STREET: 1007 MARKET
CITY: WILMINGTON
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al Similarity 51.4%;
699; Conservative
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Best Local Similarity
                                                                                                                                                      RESULT 14
US-09-758-652-15
                                                                                                                                                                                                                                                                                                                                                  NUMBER
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0; Mismatches 600; Indels
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                                                                                     1371 GGGAGAACAAGGATTGGAATATGTAGTGTTCAAGACACAC 1410
                                    GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IB PC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS SOFTWARE: MICROFSOFT WORD 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/684,651
FILING DATE: 14-0ct-2003
CLASSIFICATION: vUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UNITED STATES OF AMERICA
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-684-651-15
                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: LYNNE M. CHRISTENBURY
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                                                                                                                                                                                                                          Sequence 15, Application US/10684651
Patent No. 6828491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1551 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 302-992-5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.0%;
51.4%;
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                                                                                                                                                                                                                                                                                                             APPLICANT: ANTHONY JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. I
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Search completed: June 23, 2006, 10:41:55 Job time: 251.534 secs

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GenCore version 5.1.9
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- nucleic search, using sw model OM nucleic

Run on:

June 23, 2006, 18:12:55; Search time 2083.24 Seconds (without alignments) 8989.054 Million cell updates/sec

US-10-728-051-3 1524 Perfect score:

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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

37784340 Fotal number of hits satisfying chosen parameters:

18892170 segs, 6143817638 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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8 513 33.7 1730 8 US-10-425-114-8133 Sequence 813. 9 513 33.7 1834 8 US-10-424-599-28863 Sequence 288. 1 511.4 33.6 1458 10 US-10-409-993-14 Sequence 286. 5 512.4 33.6 1729 8 US-10-425-114-8584 Sequence 858. 5 505 33.1 1746 3 US-10-922-732-15 Sequence 15, 5 504 33.1 1746 9 US-10-922-732-15 Sequence 15, 5 504 33.1 1458 3 US-09-758-652-12 Sequence 15, 5 504 33.1 1458 3 US-09-758-652-12 Sequence 15, 5 504 33.1 1458 3 US-09-758-652-12 Sequence 15, 5 505 33.1 1458 3 US-09-758-652-12 Sequence 12, 5 504 504 504 504 504 504 504 504 504 50	Sequence 759 Sequence 16 Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 764	8 US-10-425-114-816		۳.	513	37
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4 513 33.7 1724 8 US-10-425-114-8687 Sequence 858° 513 33.7 1727 8 US-10-425-114-7603 Sequence 760° 513 33.7 1727 8 US-10-425-114-7624 Sequence 760° 513 33.7 1729 8 US-10-425-114-8133 Sequence 762° 513 33.7 1730 8 US-10-425-114-8133 Sequence 8136° 513 33.7 1834 8 US-10-424-599-28863 Sequence 288° 60° 511.4 33.6 1458 10 US-10-409-993-14 Sequence 14 Sequence 14 Sequence 15 30° 53.1 1746 3 US-10-925-114-8584 Sequence 15 50° 53.1 1746 9 US-10-922-732-15 Sequence 15 50° 53.1 1746 9 US-10-522-732-15 Sequence 15 50° 53.1 1746 9 US-10-522-732-15 Sequence 15 50° 53.1 1746 9 US-10-528-652-12 Sequence 15 50° 50° 50° 50° 50° 50° 50° 50° 50° 50	Sequence 7595 Sequence 16 Sequence 11, Sequence 12, Sequence 12, Sequence 13, Sequence 14, Sequence 16, Sequence 767, Sequence 855,	8 US-10-425-114-				2
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ALIGNMENTS

APPLICANT: Caplan, Michael
TITLE OF INVENTION: Microbial Delivery System
TITLE REFERENCE: 2002834-0100
CURRENT APPLICATION NUMBER: US/09/731,375A
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/195,035
PRIOR FILING DATE: 2000-04-06 Sequence 3, Application US/09731375A Publication No. US20030035810A1 GENERAL INFORMATION: NUMBER OF SEQ ID NOS: 3 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 3 LENGTH: 1524 ORGANISM: Arachis hypogaea US-09-731-375A-3 US-09-731-375A-3 TYPE: DNA

Gaps ö Length 1524; Indels DB 3; ., 0 Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 1 CGGCAGCAACCGGAGAACGCGTGCCAGTTCCAGCGCCTCAATGCGCAGAGACCTGAC

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Sequence 13, Appl Sequence 27, Appl Sequence 7280, Ap Sequence 8531, Ap Sequence 8592, Ap Sequence 7583, Ap

10 US-10-508-263-27 8 US-10-425-114-7280 US-10-425-114-8531 US-10-425-114-8592 US-10-425-114-7583

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34.0 34.0 34.0

	RESULT 2 US-10-228-806-5 Sequence 5, Application US/10228806 Publication No. US20030049237A1 GENERAL INFORMATION: APPLICANT: Bannon, et al. TITLE OF INVENTION: Wethods and Reagents for Decreasing Clinical Reactions TITLE OF INVENTION: to Allergy FILE REFERENCE: 2002834-0043 CURRENT APPLICATION UNMBER: US/10/228,806 CURRENT PILING DATE: 2002-08-26 NUMBER OF SEQ ID NOS: 81 SEQ ID NO 5 LENGTH: 1524 TYPE: DNA CREANISM: Arachis hypogaea US-10-228-806-5	Ouery Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 1 CGGCAGCAACCGGAGGAGAACGCGTGCCAGTTCCAGCGCTCCAATGCGCAGACCTGAC	181 Transport 181 182 182 182 183
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US-10-100-303A-89
Sequence 89, Application US/10100303A
Publication No. US20030202980A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and Reagents for TITLE OF INVENTION: to Allergy
FILE REFERENCE: 2002834-0166
CURRENT APPLICATION NUMBER: US/10/100,303A
CURRENT FILING DATE: 2002-03-18
NUMBER OF SEQ ID NOS: 138
SEQ ID NO 89
LENGTH: 1524
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100.0%; Score 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches
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                                                                           Query Match 100.0%; Score 1524; Best Local Similarity 100.0%; Pred. No. 0; Matches 1524; Conservative 0; Mismatches
; SEQ ID NO 3
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-323-3
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Publication No. US20040208894A1

GENERAL INFORMATION:

APPLICANT: Caplan, Michael J.

APPLICANT: Bottomly H., Kim

APPLICANT: Bottomly H., Kim

APPLICANT: Banks A., Hedah

TITLE OF INVENTION: Microbial Delivery System

FILE REFERENCE: 2002834-0232

CURRENT APPLICATION NUMBER: US/10/728,323

CURRENT APPLICATION NUMBER: 09/95,035

PRIOR FILING DATE: 2003-12-04

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Bottomly H., Kim
APPLICANT: Sosin B., Howard
APPLICANT: Sampson A., Hugh
APPLICANT: Sampson A., Hugh
TITLE OF INVENTION: Microbial Delivery System
TITLE OF INVENTION: Microbial Delivery System
TITLE OF INVENTION Microbial
FILE REPERENCE: 2002834-0222
CURRENT APPLICATION NUMBER: 08/10/728,051
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: 09/731,375
PRIOR PLING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 3
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Publication No. US20040234548A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                       COMPANY
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Pred. No. 3.2e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 421;
                                                                                                                                                                                                                                                                                                       NEMOURS AND
                                                                                                                                                                       APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: LBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROSOFT WORD 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE DOCKET NUMBER: BB-1071-A TELECOMMUNICATION INFORMATION:
TELEBROME: 302-992-5481
TELEFAX: 302-73-0164
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
APPLICATION NUMBER: US/09/758,652
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UNITED STATES OF AMERICA ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/019,940
                       CAGTCTCCGAGGGCTGTGGCTTAA 1593
     CAGTCTCCGAGGGCTGTGGCTTAA 1524
                                                                                                                                                                                                                                                   PROTEIN GENES
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSESE: E. I. DU PONT DE STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 30,971
                                                                                                                           Sequence 13, Application US/09758652
Patent No. US20010011377A1
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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62.8%;
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                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21
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Best Local Similarity 62.8
Matches 954; Conservative
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                                                                                          RESULT 8
US-09-758-652-13
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                                                                                                191 GIGCCGGIGTIGCCCTCTCTCGCTGCACCCTCAACCGCAACGCCCTTCGCAGACCTTCCT
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                                                           GCGCCGGCGTCGCCTCTCGCTTAGTCCTCCGCCGCAACGCCCTTCGTAGGCCTTTCT
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AGTATGTTTCATTCAAGACCAATGATAGACCCTCGATCGGCAACCTTGCAGGTGCAAACT 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AGCAGCCACAGCAAAACGAGTGCCAGATCCAACGCCTCAATGCCCTAAAACCGGATAACC 130
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                                                           CATTGTTGAACGCATTGCCGGAGGAAGTGATTCAGCAAACTTTTAACCTAAGGAGGCAGC
                                      CCGTCATAGATAACCTGCCGGAGGAGGTGGTTGCAAATTCATATGGCCTCCAAAGGGAGC
                                                                                                                  AGGCAAGGCAGCTTAAGAACAACAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                               GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS SOFTWARE: MICROFSOFT WORD 7.0A APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: BB-1071-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/684,651
FILING DATE: 14-Oct-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-684-651-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: LYNNE M. CHRISTENBURY REGISTRATION NUMBER: 30,971
                                                                                                                                                                                                                                                                                    RESULT 9
US-10-684-651-13
Sequence 13, Application US/10684651
Sequence 13, Application No. US20040064858A1
Dublication No. US20040064858A1
GENERAL INFORMATION:
APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
GARY MICHAEL FADER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: E. I. DU PONT D
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                         1427 AGAGGAGAGTTGTGGCTTA 1445
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LENGTH: 1446 base pairs
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TELEFAX: 302-773-0164
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STRANDEDNESS: single
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Matches 954; Conservative
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                                                           Length 1446;
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                                                       Query Match 34.0%; Score 517.4; DB 8; Best Local Similarity 62.8%; Pred. No. 3.2e-154; Matches 954; Conservative 0; Mismatches 421;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-757-074-13
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   TCGTGCCACACTACAACCTGAACGCAAACAGCATAATATACGCATTGAATGGACGGCCAT 1126
                                           ACGTGCAAGTCGTGGACAGCAACGGCAACAGAGTGTACGACGAGGAGGACCTTCAAGAGGGTC 1264
                                                                                                                                                                                               AATACGTGGCATTCAAGACAGACTCAAGGCCCCAGCATAGCCAACCTCGCCGGTGAAAACT 1384
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STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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APPLICATION NUMBER: US/10/757,074
FILING DATE: 14-Jan-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: UNR 14,1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROSOFT WORD 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/10757074
Publication No. US20040139502A1
GENERAL INFORMATION:
APPLICANT: ANTHONY JOHN KINNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
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1427 AGAGGAGATTGTGGCTTA 1445
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LENGTH: 1446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 302-992-5481
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INFORMATION FOR SEQ ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA
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191 GTGCCGGTGTTGCCTCTCTCGCTGCACCCTCAACCGCCTTCGCAGACCTTCGT 250
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Pred. No. 3.2e-154;
0; Mismatches 421;
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                                                                                                                                                                                                                                                                        NO: 13
  REGISTRATION NUMBER: 30,971
                       REFERENCE/DOCKET NUMBER: ETELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                     LENGTH: 1446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.8%;
Matches 954; Conservative
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                                                                   1205 ACGTGCAAGTCGTGGACAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264
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ATGGCATTGACGAGACCATTTGCACAATGAGACTTCGCCACACAACATTGGCCAGACTTCAT 946
                                                                                                                                                                   1007 CAGCCCTCTCGTGGCTCAAACTCAGTGCCCAGTTTGGATCACTCCGCAAGAATGCTATGT
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                                                                                                                                TAATACTTAGGTGGCTTGGACCTAGTGCTGAATATGGAAATCTCTACAGGAATGCATTGT
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                                          CCCCTGACATCTACAACCCTCAAGCTGGTTCACTCAAAACTGCCAACGATCTCAACCTTC
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ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: NICHT WARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SUPPRESSION OF SPECIFIC CLASSES OF SOYBEAN SEED PROTEIN GENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/757,155
FILING DATE: 14-Jan-2004
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ANTHONY JOHN KINNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/10757155 Publication No. US20040139503A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                               TELECOMMUNICATION INTERNATION:
TELECOMMUNICATION INFORMATION:
TELEFPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1446 base pairs
                                                            FILING DATE: 14-Jan-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
SOFTWARE: MICROFSOFT WORD 7.0A CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/757,667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
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Matches 954; Conservative
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                                                TCAGAATCTTGAGCCCAGATAGAAAGAGACGTGCCGACGAAGAGAGAATACGATGAAG
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CORRESPONDENCE ADDRESS:
ADDRESSEE. E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
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MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ANTHONY JOHN KINNEY
GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
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SOFTWARE: Pa
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                                                                                                                    AAAGCCAGAAAGGAAAGCGTCAGCAAGAAGAAGAAACGAAGGAGGAGGCAGCATATTGAGTG 664
                                                                                 GCTTCGCCCCGGAATTCTTGGAACATGCGTTC---GTCGTGGACAGGCAGATAGTGAGAA 721
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  ---GAGGTACTC 604
                     ACAGCCGCAGAGAACGAGCAGGACAAGAAGAAAAAAGGAAGGTGGAAACATCTTCAGCG
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                                                             ACCTAAGAGGCGAGACCGAGAGTGAAGAAGAGGGAGCCATTGTGACAGTGAGGGGGCC
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US-10-508-263-27
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                                                                                                                                    Length 1446;
                                                                                                                                                                 Indels
                                                                                                                                     DB 10;
                                                                                                                                    Score 517.4; DB 10;
Pred. No. 3.2e-154;
0; Mismatches 421;
                                                                         LOCATION: (1)..(1443)
COTHER INFORMATION: glycinin G3 subunit
US-10-508-263-27
                                                                                                                                  Query Match
Best Local Similarity 62.8%;
Matches 954; Conservative 0
LENGTH: 1446
TYPE: DNA
ORGANISM: Glycine max
PEATURE:
NAME/KEY: CDS
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Sequence 27, Application US/10508263
Publication No. US20050260754A1
GENERAL INFORMATION:
APPLICANT: BASF Plant Science GmbH
TITLE OF INVENTION: Constructs and methods for regulating gene expression FILE REFERENCE: 53262-20085.00
CURRENT APPLICATION NUMBER: US/10/508,263
CURRENT FILING DATE: 2004-09-20

Gaps

152 124

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184 272 244 332 364 364 404 424 464 484 524 544 584 604

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ATGGTATTGAAGAGACGATCTGCACCGCAAGTGCTAAAAAGAACATTGGTAGAAACAGAT 1024
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                                           144;
  Length 1673;
                                         Indels
Score 517.4; DB 8;
Pred. No. 3.4e-154;
0; Mismatches 421;
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Query Match
Best Local Similarity 62.8%;
Matches 954; Conservative
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Sequence 8531, Application WS/0040034888A1

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Law Forman Norman Sequence and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)8

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 8531
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                                                                        CAGCCTCTCGTGGCTCAAACTCAGTGCCCAGTTTGGATCACTCCGCAAGAATGCTATGT 1088
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TGGTACAAGTGGTGAATTGCTGAGTGAGAGTGTTTGATGGAGAGGCTGCAAGAGGGGC
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                                                     TAATACTTAGGTGGCTTGGACCTAGTGCTGAATATGGAAATCTCTACAGGAATGCATTGT
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Pred. No. 3.4e-154;
0; Mismatches 421;
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; OTHER INFORMATION: Clone ID: 700757865_FLI
US-10-425-114-8531
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Matches 954; Conservative (
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                                                                               1281 AGTATGTTTCATTCAAGACCCAATGATGACCCTCGAGACGAACCTTGCAGGGGGAAACT 1340
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                                       1325 AATACGTGGCATTCAAGACAGACTCAAGGCCCAGCATAGCCAACCTCGCCGGTGAAAACT 1384
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Search completed: June 24, 2006, 01:56:17 Job time: 2087.24 secs

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365 AGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTGCAGTTCCCACCGGTGTTGCTTTCT
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968; Conserv
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Sequence 21829, A
Sequence 7351, Ap
Sequence 9966, Ap
Sequence 9937, Ap
Sequence 9993, Ap
Sequence 9993, Ap
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3323, Ap
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28281,
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*

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7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

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US-10-953-349-13162
US-10-953-349-13162
Sequence 13162, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: US/10/953,349
CURRENT APPLICATION NUMBER: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 13162
LENGTH: 1746
           17, Appl
4313, Ap
18073, A
263, App
6223, Ap
81910, A
51, Appl
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16686, Ap
12987, Ap
563, App
1642, Ap
14886, A
18002, A
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Sequence 1227, Ap
                                                                                                     5982, Al
16686, I
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US-10-953-349-4313

US-10-517-441-263

US-10-419-902-623

US-11-217-529-81910

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US-11-217-529-81910

US-11-217-529-81910

US-11-217-529-6042

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Pred. No. 7.8e-149;
0; Mismatches 425;
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llarity 62.7%;
Conservative
max
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DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 1439 ACACTTTCAACCTAAAAGCCAGCAGGCCAGGCAGATAAAGAACAACAACCATTTCAAGT 1498
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4.7e-146;
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                                                                                                                           ; Sequence 13154, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SEQ ID NO 1154
                                                                                                                                                                                                                                                                                                                                                                                      Score 504;
Pred. No. 4
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Best Local Similarity 62.0%;
Matches 943; Conservative
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TITLE OF INVENTION: SEQUENCE-DETERMINED DN
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUSZ
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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Publication No. US20060107345A1
GENERAL INFORMATION:
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GAGACGAGCACCAGCAACTTCACCAGTTCCACCAAGGTGAATGTAATCGCAGTGCCAGCTG
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                                                     GAACACGGAGCAAGAGTTCTTAAGGTACCAGCAACAAGCAGACAAAGCAGACGAAGAAG
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                                                                                     GAGTAGCCCACTGGCTACATAGCATGGTGATTCTCCTGTGGTTGCTTTCACTGTCATCG
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITLLE OF INVENTION: FULL-LENGTH PLANT CONA AND USES THEREOF
FILE REFERENCE: MOA-AQ205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-06-29
PRIOR FILING DATE: 2003-06-29
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARR: Patentin Ver. 2.1
 TGGCAGGGGAAGCAGAGGCAGGGGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7351, Application US/10449902; Publication No. US20060123505A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa
UUBLICATION INFORMATION:
DATABASE ACCESSION UNMER: AK064478
DATABASE ENTRY DATE: 2001-12-06
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Matches 661; Conser
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LENGTH: 1768
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Sequence 9937, Application US/10449902

Bublication No. US20060123505A1

GENERAL INPORMATION:

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The Institute of Agrobiological Sciences.

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CRGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107285
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9937
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Best Local Similarity 56.8
Matches 295; Conservative
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITLE OF INVENITON: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A020SY1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2002-05-29
PRIOR PLING DATE: 2002-05-39
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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1541 TAGGCTTTCAAGGGAGGACTCTAGGCATGTAAAGTTCAAC 1580
                                                                                                                                                                                                          Sequence 9966, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATABASE ACCESSION NUMBER: AK107314
DATABASE ENTRY DATE: 2002-08-28
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11.0%;
Best Local Similarity 54.4%;
Matches 362; Conservative
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LENGTH: 1764
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                                                                                                                                                                                       Sequence 9995, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Rio-oxiented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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Pred. No. 2.5e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
1422 GAAGCTAGGAGGCTCAAGCACAACA 1446
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107343
DATABASE BUTRY DATE: 2002-08-28
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Best Local Similarity 52.1%;
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LENGTH: 1650
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APPLICANT: National Institute of Parchiology Research Advancement Institution.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
ITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPERENCE: MOA-AD2051-US
CURRENT APPLICATION NUMBER: 10210/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 8.2e-35;
0; Mismatches 225; Indels
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                                                                                       GCCTCCAAAGGGAGCAGGCAAGGCAGCTTAAGAACAACA
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Publication No. US20060123505A1
GENERAL INFORMATION:
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DATABASE ENTRY DATE: 2002-08-28
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Matches 280; Conservative
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US-10-449-902-9923
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LENGTH: 1655
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; OTHER INFORMATION: Leg1 coding sequence
US-11-284-201-4
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; Sequence 4, Application US/11284201
; Publication No. US20060130184A1
; GENERAL INFORMATION:
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                                                                                                                                                                    APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US 2003-05-29
PRIOR FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-012-11
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1406 CGTATCGCATCTCAAGGGAGCAAGCCCGAAGCCTCAAGAACAACA 1450
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Pred. No. 2.5e-32;
0; Mismatches 322; Indels
                                                              RESULT 9
US-10-449-902-9890
S. Sequence 9890, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK107238
DATABASE ENTRY DATE: 2002-08-28
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Best Local Similarity 51.3%;
Matches 343; Conservative
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1322 GACCAATGCAAACTCCATGGTGAGCCACCTTGCAGGGAAGAACTCAATATTCCGTGCCAT 1381
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                                                                        1401 GCCGGAGGAGGTGGTTGCAAATTCATATGGCCTTCCAAAGGGAGCAGGCAAGGCAAGGCTTAA
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Best Local Similarity 56.5%; Pred. No. 4.3e-31;
Matches 247; Conservative 0; Mismatches 190; Indels
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APPLICANT: Jung, Rudolf
TITLE OF INVENTION: Seed-Preferred Regulatory Elements
FILE REPERENCE: 1650
CURRENT APPLICATION NUMBER: US/11/284,201
CURRENT PILING DATE: 2005-11-21
PRIOR APPLICATION NUMBER: 60/634,914
PRIOR FILING DATE: 2004-12-10
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 4
LENGTH: 1654
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RESULT 13
US-11-260-842-1/c
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Sequence 7668, Application US/10449902
| Pubblication No. US20060123505A1
| GENERAL INFORMATION:
| APPLICANT: National Institute of Agrobiological Sciences.
| APPLICANT: National Institute of Payancement Institution.
| APPLICANT: The Institute of Physical and Chemical Research,
| APPLICANT: The Institute of Physical and Chemical Research,
| TILLE OF INVENTION: FULL.LENGTH PLANT CDNA AND USES THEREOF
| TILLE REFERENCE: MOA-AO2051-US
| CURRENT APPLICATION NUMBER: US 2003-05-29
| PRIOR PLING DATE: 2003-05-30
| PRIOR FILING DATE: 2002-05-30
| PRIOR PLING DATE: 2022-05-30
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Pred. No. 4.5e-23;
0; Mismatches 273; Indels
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DATABASE ACCESSION NUMBER: AK105316
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.8%;
Matches 271; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAG 1461
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APPLICANT: Vance, Jeffrey M.
APPLICANT: Vance, Jeffrey M.
APPLICANT: Vance, Jeffrey M.
APPLICANT: Kraus, William B.
APPLICANT: Goldschmidt, Pascal J.
APPLICANT: Goldschmidt, Pascal J.
APPLICANT: Goldschmidt, Pascal J.
APPLICANT: Goldschmidt, Pascal J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
FILE REPERBORE: 5405-347
CURRENT APPLICATION NUMBER: US 60/662,447
PRIOR APPLICATION NUMBER: US 60/662,447
PRIOR FILING DATE: 2004-10-27
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHLIN Version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1190 TGAGGGGACGGGCTCACGTGCAAGTCGTGGACAGCAACGGCAACAGAGTGTACGACGAGG 1249
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                                                                                                                    APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Payrology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TILLE OF INVENTION: PULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPREBENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-3383870
PRIOR APPLICATION NUMBER: JP 2002-3383870
PRIOR SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 3323
LENGTH: 1478
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                        Sequence 3323, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK061022
DATABASE ENTRY DATE: 2001-12-06
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ORGANISM: Homo sapiens
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Best Local Similarity
US-10-449-902-3323
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1468 A 1468
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US-11-217-529-76067
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                                                                                                                                                                         AGAGGAATACGATGAAGATGAATATGAATACGATGAAGAGGATAGAAGGCGTGGCAGGGG 947
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Sequence 152, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
FILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFRENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT TILING DATE: 2002-05-39

PRIOR FILING DATE: 2002-05-39

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SCOUTMARE OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                                  1008 CATTGGTAGAAACAGATCCCCTGACATCTACAACCCTCAAAGCTGGTTCACTCAAAACTGC
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45.8%; Pred. No. 0.022;
tive 0; Mismatches 163; Indels 0
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DATABASE ENTRY DATE: 2001-12-06
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Matches 138; Conservative
                                          Conservative
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PUBLICATION INFORMATION
                      al Similarity
137; Conserv
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LENGTH: 1364
Query Match
Best Local S
Matches 137
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1408 GAGGTGGTTGCAAATTCATATGGCCTCCAAAGGGAGCAGGCAAGGCAGCTTAAGAACAAC 1467
                                                            1078 daddidergdaggegregiterrenaegggaegeceggadargdagdagererreeggregna 1137
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAWURA, NORHHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: KUJIWURA, TOMOKO
APPLICANT: FUJIWURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Pred. No. 0.028;
0; Mismatches 60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 5-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                         Sequence 76067, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
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Job time: 38.1692 secs
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US-11-217-529-76067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.6%;
Best Local Similarity 58.8%;
Matches 87; Conservative
   DB 7; Length 261789;
2.7%; Score 40.4; DB 7; Length 2
48.9%; Pred. No. 0.54;
Live 0; Mismatches 141; Indels
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